	
Ή	
<u> </u>	
\mathbb{P}	
\perp	

Clone ID	Clofibrate	Clone ID Clofibrate Fenofibrate	Captobril	Enalapril	Dexamethasone	DES	MCA	LY294002	LY294002 Ins/LY294002
26474			•	•	-4.2	2.6			
63038	-3.95	-2.9	-3.16	-2.97	-2.36				
72713							3 2.96		
86390	-2.83								
118501			4.36	90.9	2.79		4.54		-2.4
121785							3.3		
136073			(6			3.1		
160822			2.5	2.39					
167081					2.14	2.85		-3 38	
211389			-2.52		o.C-	C0:7			
237027					-2.85				
293477						2.83			
271299									2.91
279249							•	t	-2.15
279898				4.08			5.48	6.7	
280932	-2.8	-2.67				•			
293477						2			
311346							4.59		
318486							4.11		, ,,
341884	-2.32								-3.33
348143									Ţ
388964									2.88
407032	-3.05								
408886							4.93		
419492									2.47
437481		2.44				2.24			
442723									2.51
443991		2.47				2.62			
450856		2.49					2.89		
452321		m					4.3		
454839							3.4	77.4	67.0
459372								4.03	60.2

	Clofibrate	Clofibrate Fenofibrate	Captopril	Enalapril	Dexamethasone	DES	MCA	LY294002	LY294002 Ins/LY294002
460779	07.7						2.41		
480791		-2.27							
481402							3.22		
510056						2.73	5.65		
511448							3.05		
560115							-2.61		
604019							3.28		
630625	2.53	3.95	2.81	2.51	2.52		2.25		
669498							-2.97		
701484							2.51		
758192	3.11								
773154									-2.39
818192	2.87								
872017							2.85		
891322						3.81			
963536									2.93
970905		-4.06				2.25			
990375					-2.5				
1213932									6.31
1259841									3.15
1272483						2.51			•
1306814									2.83
1308112	2.19			2.14			2.28	!	
1315663	-3.18	-4.02	-2.84				,	-3.27	
1316801							3.38		
1326255			!			-2.7			
1368834			2.47	2.43					
1379063	-2.38		4	-2.44	-3.42		-3.63		
1381654			1.57		2.57		2.64		
1395143									3.09
1435374									3.67
1441245					-2.3				
1448718	-2.95		-3.93	-3.91	-3.1				
1454436							2 93		70.7
1474/641									

TABLE 1

Clone ID	Clofibrate	Clofibrate Fenofibrate	Captopril	Enalapril	Dexamethasone	DES	MCA	LY294002 Ins/LY294002	LY294002
145//18	(76.7
1464613	-2.39				,			•	
1468660					-3.3			-2.28	;
1482116									3.44
1495382									-2.77
1500245									2.92
1511658	-3.56								
1519431			2.36						
1519683	-2.12								
1522880							2.74		,
1530595									3.52
1559665	-4.058								
1559756			1.56		2.47				
1560906							3.13		ć
1577614									-3.3
1616783					2.55		2.63		
1619292	-3.07	s-	-4.3		4.4		-2.8		
1619980									-2.97
1623214					-2.25		-3.12		
1630990					2.86		3.34		
1696224	11.91		3.28	3.97	2.83		4.4		
1705208		2.83							
1711151	2.4		3.05	2.48					
1732221									-2.85
1756875							2.99		
1786554					2.66		2.67		,
1822716							,		2.45
1833362					-3.7		-2.33		
1834236					-2.3				
1838114									
1845046	-2.5							-	
1846209			1.81		2.2				
1846463	3.62	6.58							
1861456				-2.51					
1867614									5.81
1869130	_								-7.17

TABLE 1

LY294002 Ins/LY294002	-2.43 3.63 -2.57								,	-4.16					-3.56		5.55			ì	2.70	700	2.94 7.0	7.7			2.61	-2.41			3.4		
LY294002													-3.45	-2.46																			
MCA		-3.07					2.93						-2.51	2.46					-2.67	2.97	,	3.83			(2.32		0	2.72			2.44	
DES								-2.13											2.97											-2.39			
Dexamethasone		-2.5											-3.35	2.44		2.8	2.91			3.25		2.66		i	-2.51	2.3							
Enalapril							3						-2.75	2.27				-3.1				3.71											
Captopril							3.25							2.99				-3.33	-2.61			3.89											
Fenofibrate												8.9	-2.42	2.31	5.46			-3.12	-3.4			4.6							ļ	-2.7			
Clofibrate Fenofibr			2.7	-2.59	3.03	2.94	2.73		-2.52		-2.8	3.78		2.7	2.5			-2.76				8.29											2.48
Clone ID	~ ~ ~	1890576	1890791	1920215	1922468	1926883	1930235	1956982	1958226	1963081	1966517	1969563	1975268	1998269	2042056	2046717	2048551	2055569	2055867	2120743	2121863	2123516	2132285	2132774	2160794	2195427	2201708	2208780	2232658	2234853	2242817	2252107	2273944

TABLE 1

ofibrate	Clofibrate Fenofibrate	Captopril	Enalapril	Dexamethasone	DES	MCA	LY294002 Ins/LY294002	Ins/LY294002
						-2.88		
				0	-2.34	08.6		
				01.7		70.7		
	-4.5	-2.71						
	-2.87							
								-2.23
								-2.83
	-2.5							
		-2.15						
	-2.35							
								-2.4
				-2.8				
								2.22
						3.07		
	4.47		3.82	3.93		3.67		17.42
								3.35
								4.03
								2.88
								2.65
						3.21		
								2.51
					-2.49			
					2.1			
						2.42		
	-3.2							
								2.31
								4.58
				2.21		2.25		
						3.09		
						2.68		
						2.45		

LY294002 Ins/LY294002	33.5	-2.72	<u> </u>	i,	-3.IS	2.67			2.43	×	3.4			7	6.47	3.13		2.35	3.07	1	7.63		-2.67		
LY294002		-3.37																			-				
MCA	4.31	C7:7	2.96	2.44	2.48	-3.2	2.2	2.56		-4.29		-3.43				7 27	3.04						;	3.03	
DES																	2.1								
Dexamethasone	4.93		ĸ	>								-2.95	-2.63	,	4.32						90	ì		7.4.7	14.7-
Enalapril	4.13						2.51					-4.67			4.73	7 33	CC:-7								
Captopril	4.03	-2.01	2.29				2.46			-2.38		-5.21			5.14										
Clofibrate Fenofibrate	4.75	-3.17												-2.89				2.44							
Clofibrate	2.8	-2.79					2.54	-2.38				-3.1			4			2.94		2.4		2.57			
Clone ID	2757583	2769888	2820337	2825358	2830828 2831490	2860918	2884613	2890336 2891601	2899419	2912637	2912830	2921991	2925373	2929484	2933775	2953987	2955105	2957205	299102 <i>/</i> 2992044	2999855	3026540	3038508	3070625	3074113	3084204

Πĺ
BI
\forall

LY294002 Ins/LY294002	2.53	7.45	3.07	-2.86			, i	2.54					4.11						77.0	2.40										
LY294002																	4.2						-4 3	÷						
MCA 3.02					!	2.67		3 73	C7:C	65.7					2.3	2.7		2.77	2.62			3.24		2 73	7.63	3.55		2.44		2.64
DES								7	4 .7																	2.99				
Dexamethasone	7.0						-3.67					•	-2.4										2 17	77.7						2.45
Enalapril																														
Captopril										2.89	i				2,62							ć	-2.03		2 78					
Clofibrate Fenofibrate								i	7.55		73.0	/ 5.7-																		
Clofibrate					-3.24			i	7.71						-3.15						-2.53						. C-		-3.55	
	3109384 3120209	3121871	3123731	3129338	3136857	3158828	3170010	3208425	3222802	3225977	3710170	27/7/02	3284411	020000	3380034	3407653	3427373	3472927	3493381	3493710	3494714	3606046	36/966/	3/15059	3792988	2010422 4019706	4066764	4070979	4087621	4091186

LY294002 Ins/LY294002						-2.14																			
LY294002										2.45															
MCA 3.55		7.13	3.03	2.3	2.73	-2.54	2.4	2.68	2.53			3.57				2.36	2.33	2.47	2.54				•	2.26	
DES						5.66					-2.21									-2.3			-2.63		
Dexamethasone								2.86															2.63		
Enalapril										3.02															
Captopril 2.88																									
Fenofibrate						-3.14				2.53															
Clofibrate Fenofib	2.18		8.12			-3.47							-2.38								-2.67				2.38
lone ID 4092112 4107126	4110976	4203937	4246966	4254855	4284384	4287327	4403805	4508879	4549259	4556538	4715924	4721130	4795635	5047895	5077219	5093071	5102731	5266015	5266376	5293028	5398014	5398701	5399371	5512044	5541949

TABLE 2

CLONE ID	NUCLEOID E SEQ ID NO:	NUCLEOTID E TEMPLATE ID	PROTEIN SEQ ID NO:	PROTEIN TEMPLATE ID
26474	1	220060.4	······································	
60123	2	016238.1		
63038	3	1266683.1		
72713	4	129384.1c		
85606	5	3201389CB1	6	3201389CD1
86390		086390CB1	8	086390CD1
118501	9	1102322.16		
118501	10	1545176CB1	11	1545176CD1
121785	12	978222.4		
121785	13	978222.5		
136073	14	1720920CB1	15	1720920CD1
160822	16	1857017CB1	17	1857017CD1
3493710	16	1857017CB1	17	1857017CD1
167081	18	2114865CB1	19	2114865CD1
172023	20	2700132CB1	21	2700132CD1
2470485		2700132CB1	21	2700132CD1
211389	22	238349.2		
211389		238349.4c		
237027		402917.3c		
259054	25	406330.1		
271299	26	2516070CB1	27	2516070CD1
2517386	26	2516070CB1	27	2516070CD1
279249	28	167507CB1	29	167507CD1
279898	30	3860413CB1	31	3860413CD1
3121871	30	3860413CB1	31	3860413CD1
280932	. 32	3393861CB1	33	3393861CD1
293477		2517374CB1	35	2517374CD1
311346	36	030850.7		
318486	37	237416.12c		
318486	38	237416.14		
341884	. 39	1269631CB1	40	1269631CD1
348143	41	961189CB1	42	961189CD1
388964	. 43	246946.1		
389362	44	017958.1		
407032	45	985556.1		
408886	46	476301CB1	47	476301CD1
419492	48	996427.2		
437481	49	2989375CB1	50	2989375CD1
442723	51	236359.2		
443991	52	011112.1c		
450856	53	198268.1		
452321	54	978740.3		
454839	55	400197.1		
459372		235687.5c		
460779		2797839CB1	58	2797839CD1
462069		978690.6		
480791		348072.5		
481402		085596CB1	62	085596CD1
510056	63	103917 CB 1	64	103917CD1
511448	65	3603037CB1	66	3603037CD1

560115	67	088564CB1	68	088564CD1
604019	69	040429.1		
630625	70	407096.2	•	
669498	71	209265.54		
701484	72	701484CB1	73	701484CD1
758192	74	251859.2		
773154	75	3766715CB1	76	3766715CD1
818192	77	2049950CB1	78	2049950CD1
818192	79	231588.6c	, 0	201775002
872017	80	152298.2		
891322	81	199507.1		
963536	82	1434821CB1	83	1434821CD1
970905	84	289671.27	03	1434021001
990375	85	1282225CB1	86	1282225CD1
1213932	87	263336.57	80	1202223CD1
1259841	88	464689.40		
1272483	89	155943.1		
1306814	90	243794.19c		
1306814	91	243794.23	22	1.50000.501
1308112	92	159309CB1	93	159309CD1
1315663	94	1273641CB1	95	1273641CD1
1316801	96	403717.1		
1326255	97	047593.1		
1368834	98	347055.4		
1379063	99	898899.11		
1379063	100	898899.32		
1381654	101	2047630CB1	102	2047630CD1
1395143	103	1039889.8		
1435374	104	1272969CB1	105	1272969CD1
1441245	106	282397.85c		
1441245	107	282397.94		
1448718	108	1448817CB1	109	1448817CD1
1454436	110	1100769.2		
1457424	111	332521.1		
1457718	112	225080.16		
1464613	113	334851.5		
1468660	114	995529.7		
1468660	115	995529.8		
1482116	116	201851.1		
1495382	117	059509CB1	118	059509CD1
1500245	119	481231.14		
1511658	120	280276CB1	121	280276CD1
1519431	122	4675668CB1	123	4675668CD1
1519683	124	153825.1		
1522880	125	403484.2c		
1522880	126	1459432CB1	127	1459432CD1
1530595	128	1096583.1		
1559665	129	516300CB1	130	516300CD1
1559756	131	627856CB1	132	627856CD1
1560906	133	1823159CB1	134	1823159CD1
1577614	135	232567.4		
1616783	136	218419.1		
1619292	137	1630551CB1	138	1630551CD1

1619980	139	360961.19		
1623214	140	809809CB1	141	809809CD1
1630990	142	2558815CB1	143	2558815CD1
1696224	144	242010.16		
1696224	145	1678695CB1	146	1678695CD1
1705208	147	988653.1		
1711151	148	1250434CB1	149	1250434CD1
1732221	150	236196.3		
1756875	151	442308.1		
1786554	152	060957.1		
1822716	153	014284CB1	154	014284CD1
1833362	155	1095192.1		
1834236	156	233003.20		
1834236	157	1911808CB1	158	1911808CD1
1838114	159	978276.8		
1845046	160	405844.21		
1845046	161	405844.22		
1846209	162	2705515CB1	163	2705515CD1
1846463	164	2023119CB1	165	2023119CD1
1861456	166	1000084.27		
3679667	166	1000084.27		
1867614	167	220134.1		
1869130	168	216331.1		
1871340	169	206044.1		
1874037	170	382906.16		
1874307	171	331306.1		
1890576	172	1094829.20		
1890576	173	1094829.38		
1890791	174	1135580.4		
1920215	175	196623.3		
1922468	176	048488.32		
1926883	177	2767012CB1	178	2767012CD1
1930235	179	1651724CB1	180	1651724CD1
1956982	181	206397.1		
1958226	182	461707.40		
1963081	183	2706645CB1	184	2706645CD1
1966517	185	474372.7		
1969563	186	3592543CB1	187	3592543CD1
1975268	188	048612.12c		
1975268	189	048612.13		
1998269	190	245259.16		
2042056	191	522433CB1	192	522433CD1
2046717	193	1040667.43		
2048551	194	2048551CB1	195	2048551CD1
2055569	196	1969731CB1	197	1969731CD1
2055867	198	1326983.14		
2120743	199	2120743CB1	200	2120743CD1
2121863	201	3551330CB1	202	3551330CD1
2123516	203	1440032CB1	204	1440032CD1
2132285	205	1000133.1		
2132774	206	4020439CB1	207	4020439CD1
2160794	208	2507087CB1	209	2507087CD1
2195427	210	239996.1		

2201708	211	1097380.1		
2208780	212	021524.2c		
2208780	213	021524.9	•	
2232658	214	253987.16		
2234853	215	344553.1		
2241825	216	410785.1		
2242817	217	237623.6		
2252107	218	076047.1		
2273944	219	1099500.15		
2273944	220	1099500,18		
2278688	221	2278688CB1	222	2278688CD1
2293496	223	380283.1		
2311213	224	1720847CB1	225	1720847CD1
2343348	226	333776.1c		
2352645	227	3478236CB1	228	3478236CD1
2360580	229	147541.17		
2365335	230	331120.16c		
2382192	231	575983CB1	232	575983CD1
2382195	233	413268.6		
2383269	234	1989186CB1	235	1989186CD1
2394990	236	337448.1c		.,0,10002.
2399162	237	228304.19		
2446289	238	420527.25		
2448149	239	998034.3		
2453558	240	474165.26		
2495131	241	697785CB1	242	697785CD1
2511277	243	346209.3		
2513883	244	167772CB1	245	167772CD1
2514988	246	2514988CB1	247	2514988CD1
2516070	248	481231.16		,
2516070	249	481231.17		
2516104	249	481231.17		
2516261	249	481231.17		
2516448	249	481231.17		
2517254	250	1045853.2		
5398014	250	1045853.2		
2520894	251	336615.1		
2527879	252	1328423.2		
2545486	253	085282.1		
2550767	254	1081605.3		
2579218	255	1053517.1		
2607921	256	480169.76		
2636043	257	2636043CB1	258	2636043CD1
2641522	259	2993696CB1	260	2993696CD1
2660756	261	240518.21		
2660756	262	240518.34		
2663164	263	001322.4c		
2675232	264	350502.3		
2675232	265	350502.4c		
2695371	266	253783.3		
2708055	267	085119.1		
2740665	268	902559.1		
2756333	269	4113161CB1	270	4113161CD1

2757583	271	2757583CB1	272	2757583CD1
2765271	273	198317.1		
2769888	274	1508254CB1	275	1508254CD1
2813255	276	474691.3		
2820337	277	2457215CB1	278	2457215CD1
2822027	279	201395.4c		
2825358	280	233189.21		
2830828	281	196606.6c		
2830828	282	196606.8c		
2831490	283	1040190.3		
2860918	284	1427459CB1	285	1427459CD1
2879068	286	480453.16c		
2884613	287	1095604.1		
2890336	288	241291.28		
2891601	289	230611.1		
2899419	290	3993708CB1	291	3993708CD1
2899419	292	1000133.12	=/:	
2912637	293	400253.17c		
2912637	294	400253.5		
2912830	295	030882CB1	296	030882CD1
2921194	297	898779CB1	298	898779CD1
2921991	299	3727408CB1	300	3727408CD1
2925373	301	984236.1c	500	3727 100027
2925373	302	984236.2c		
2929484	303	348082.5		
2929484	304	348082.7		
2933775	305	1097910.1		
2953987	306	246841.1		
2955163	307	351241.1		
2956444	308	2790762CB1	309	2790762CD1
2957205	310	2253717CB1	311	2253717CD1
2991027	312	2655184CB1	313	2655184CD1
2991027	314	363000.9c	0.0	200010.02.
2992044	315	232818.15		
2999855	316	347781.10		
2999855	317	2477616CB1	318	2477616CD1
3026540	319	360532.1	*	
3026540	320	360532.9		
3028719	321	110245.1		
3038508	322	478620.53		
3038508	323	1813444CB1	324	1813444CD1
3070625	325	474588.21	52.	1010111001
3074113	326	407838.1		
3084204	327	994387.19		
3108506	328	347796.7		
3109384	329	406498.4c		
3120209	330	3346307CB1	331	3346307CD1
3121380	332	4005778CB1	333	4005778CD1
3123731	334	995575.17	555	.00277002
3128810	335	863406CB1	336	863406CD1
3129338	337	413864.17	550	303.00021
3136857	338	350106.16		
3158828	339	399785.1		
2120020	ردد	375103.1		

3170010	340	010498.19		
3208425	341	255824.39		
3208425	342	2706606CB1	343	2706606CD1
3222802	344	118006.1		
3225977	345	1039889.26		
3240708	346	481480.7		
3272165	347	662575CB1	348	662575CD1
3284411	349	027619.3	• . •	
3345528	350	235447.5		
3380034	351	331104.2		
3381870	352	348390.2		
3407653	353	127004.1		
3427373	354	026190.1		
3472927	355	250330.1		
3493381	356	480375.28		
3494714	357	364726.10		
3494714	358	364726.12		
3606046	359	1505038CB1	360	1505038CD1
3715059	361	903508.12	200	1505050021
3792988	362	346716.17c		
3792988	363	346716.21c		
3815422	364	330776.1		
4019706	365	407999.1c		
4066764	366	1719478CB1	367	1719478CD1
4070979	368	351157.2		
4087621	369	088957CB1	370	088957CD1
5398701	369	088957CB1	370	088957CD1
4091186	371	980446.1		
4092112	372	198827.1		
4107126	373	1102297.22		
4110976	374	215112.1		
4203937	375	171495.1		
4246966	376	242010.43		
4254855	377	5834958CB1	378	5834958CD1
4284384	379	335648.1c		
4287327	380	333840.1		
4403805	381	480885.2		
4508879	382	998106.8c		
4549259	383	400701.4		
4556538	384	1100320.4		
4715924	385	246727.11		
4715924	386	246727.17		
4721130	387	1102322.12c		
4721130	388	1102322.18		
4795635	389	2070610CB1	390	2070610CD1
5047895	391	336733.3		
5077219	392	1326902.13		
5077219	393	1326902.6		
5093071	394	013521.16		
5102731	395	985369.1		
5266015	396	002455.1		
5266376	397	372647.1		
5293028	398	208075.1		

5399371	399	209279.1
5512044	400	381058.1
5541949	401	046977 1

ngglaciae invent

TABLE 3

			g286008 0 Human mRNA for KIAA0020 gene, complete cds.	g286008 0 Human mRNA for KIAA0020 gene, complete cds.	g4107230 3.00E-34 Human mRNA for lipophilin B.	Incyte Unique	Incyte Unique	g1232174 0 Human mRNA for transketolase-like protein (2418 bp).	74	g179892 0 Human cAMP phosphodiesterase PDE7 (PDE7A1) mRNA, complete cds.	Incyte Unique	Incyte Unique		103	g4337095 0 Human MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G5b, G6d, G6e, G6f, BAT5, G5b, CSK:		g1457944 5.00E-10 Human desmoglein 3 gene, promoter region.		g189421 0 Human proliferating-cell nucleolar protein P120 mRNA, complete cds.	g189421 0 Human proliferating-cell nucleolar protein P120 mRNA, complete cds.	g3287264 e-145 Rattus norvegicus mRNA for STOP protein.			g184391 0 Human histidine-rich glycoprotein mRNA, complete cds.	0				g1778716 0 Human chemokine exodus-1 mRNA, complete cds.	g1778716 0 Human chemokine exodus-1 mRNA, complete cds.							odo14599 O Human mRNA: cDNA DKFZp564A126 (from clone DKFZp564A126); partial cds.
			g28(g28(g41(g12.	g12.	g17	_	_		g318	g43.		g14.			_	g32	828	818	g18,	818	g18		_	g17	g17		g12	g21	g59	g59	gll	
237416.14	1269631CB1	1269631CDI	961189CB1	961189CD1	246946.1	017958.1	985556.1	476301CB1	476301CD1	996427.2	2989375CB	2989375CD	236359.2	011112.1c	198268.1	978740.3	400197.1	235687.5c	2797839CB	2797839CD	9.069816	348072.5	085596CB1	085596CD1	103917CB1	103917CDI	3603037CB	3603037CD	088564CB1	088564CD1	040429.1	407096.2	209265.54	701484CB1	701484CDI	251859.2	3766715CB1

roalowe broom

 0 Human mRNA; cDNA DKFZp564A126 (from clone DKFZp564A126); partial cds. 0 Human gamma-glutamylcysteine synthetase (GCS) mRNA, complete cds. 0 Human gamma-glutamylcysteine synthetase (GCS) mRNA, complete cds. 0 Human gamma-glutamylcysteine synthetase (GCS) mRNA, complete cds. Incyte Unique Incyte Unique 	 0 Human pS2 mRNA induced by estrogen from Human breast cancer cell line MCF-7. 0 Human pS2 mRNA induced by estrogen from Human breast cancer cell line MCF-7. 0 Human GPx-3 mRNA for plasma glutathione peroxidase. 	 0 Human liver fatty acid binding protein (FABP) mRNA, complete cds. 0 Human liver fatty acid binding protein (FABP) mRNA, complete cds. 0 Human metallothionein-le gene (hMT-le). 0 Human CST3 gene for cystatin C. 0 Human mRNA: cDNA DKFZp434K098 (from clone DKFZp434K098); partial cds. 	 0 Human ribosomal protein S29 mRNA, complete cds. 0 Human ribosomal protein S29 mRNA, complete cds. 0 Human Ki nuclear autoantigen mRNA, complete cds. 0 Human Ki nuclear autoantigen mRNA, complete cds. 	Incyte Unique Incyte Unique Incyte Unique Incyte Unique	 0 Human 3-hydroxy-3-methylglutaryl CoA synthase mRNA, complete cds. 0 Human hepatocyte growth factor-like protein mRNA, complete cds. 0 Human hepatocyte growth factor-like protein gene, complete cds. 0 Human asparagine synthetase mRNA, complete cds. 0 Human asparagine synthetase mRNA, complete cds. 0 Human cytoskeletal gamma-actin gene, complete cds. 	 0 Human mRNA for XPAC protein. 0 Human mRNA for XPAC protein. 0 Human D15F37 pseudogene, S3 allele, mRNA sequence. 0 Human mRNA for KIAA0393 protein, partial cds. 0 Human insulin-like growth factor binding protein mRNA, complete cds. 0 Human insulin-like growth factor binding protein mRNA, complete cds. 0 Human mRNA for ribosomal protein S26. Incyte Unique 0 Human 2,3-oxidosqualene-lanosterol cyclase mRNA, complete cds. 0 Human mRNA; cDNA DKFZp434P1550 (from clone DKFZp434P1550); partial cds.
g4914599 g183038 g183038 g183038	g35706 g35706 g31896	g182355 g182355 g187538 g30257	g550026 g550026 g510689	b	g410027 g183976 g1311660 g179099 g178042	g286028 g286028 g3660662 g6683696 g183117 g296451 g951313
3766715CD1 2049950CB1 2049950CD1 231588.6c 152298.2 199507.1	1434821CB1 1434821CD1 289671.27	1282225CB1 1282225CD1 263336.57 464689.40 155943.1	243794.19c 243794.23 159309CB1	1273641CB1 1273641CD1 403717.1 047593.1	347055.4 898899.11 898899.32 2047630CB1 2047630CD1 1039889.8	1272969CB1 1272969CD1 282397.85c 282397.94 1448817CB1 1100769.2 332521.1 225080.16
76 77 78 79 80 81	83 84 84	85 88 88 89	90 91 93	94 95 96	98 99 100 101 102	104 105 106 107 108 110 111 111

TABLE 3

0 Human mRNA for CDC2 delta T, complete cds.	0 Human CDC2 gene involved in cell cycle control.	0 Human echinoderm microtubule-associated protein homolog HuEMAP mRNA, complete cds.	0 Human TNF-related apoptosis inducing ligand TRAIL mRNA, complete cds.	0 Human TNF-related apoptosis inducing ligand TRAIL mRNA, complete cds.	0 Human mRNA for apolipoprotein AI (apo AI)=.	0 Human fibrinogen alpha subunit and fibrinogen alpha subunit precursor, genes, complete cds.	0 Human fibrinogen alpha subunit and fibrinogen alpha subunit precursor, genes, complete cds.	0 Human bystin mRNA, complete cds.	0 Human bystin mRNA, complete cds.	0 Human stromelysin-3 mRNA.	0 Human somatostatin receptor-like protein (GPR24) gene, complete cds.	0 Human somatostatin receptor-like protein (GPR24) gene, complete cds.	0 Human somatostatin receptor-like protein (GPR24) gene, complete cds.	9.00E-96 Human gene for cytochrome P(1)-450.	0 Human CD94 protein mRNA, complete cds.	0 Human CD94 protein mRNA, complete cds.	0 Human tyrosyl-tRNA synthetase mRNA, complete cds.	0 Human tyrosyl-tRNA synthetase mRNA, complete cds.	0 Human myotubularin (MTM1) mRNA, complete cds.	0 Human myotubularin (MTM1) mRNA, complete cds.	0 Human follistatin gene, exons 1-5.	Incyte Unique	0 Human mRNA for cytochrome c1.	0 Human mRNA for cytochrome c1.	0 Human methionine adenosyltransferase alpha subunit gene fragment.	0 Human BRCA1-associated protein 2 (BRAP2) mRNA, complete cds.	0 Human BRCA1-associated protein 2 (BRAP2) mRNA, complete cds.	0 Human gamma-aminobutyraldehyde dehydrogenase mRNA, complete cds.	0 Human gamma-aminobutyraldehyde dehydrogenase mRNA, complete cds.	0 Human MHC class III HSP70-1 gene (HLA), complete cds.	0 Human genomic DNA, chromosome 6p21.3, HLA Class I region, section 2/20.	0 Human genomic DNA, chromosome 6p21.3, HLA Class I region, section 2/20.	0 Human mRNA for early growth response protein 1 (hEGR1).	0 Human MOP1 mRNA, complete cds.	0 Human MOPI mRNA, complete cds.	0 Human genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung c	0 Human homeodomain protein (Nkx2.2) gene, exon 2 and complete cds.
g3126638	g29838	g2104768	g1149557	g1149557	g28771	g182406	g182406	g1160618	g1160618	g456256	g1737178	g1737178	g1737178	g30340	g1098616	g1098616	g2665518	g2665518	g1378039	g1378039	g182718		g30302	g30302	g896282	g3252871	g3252871	g1049218	g1049218	g188487	g5926690	g5926690	g31129	g1144012	g1144012	g4003383	g3955193
995529.7	995529.8	201851.1	059509CB1	059509CD1	481231.14	280276CB1	280276CD1	4675668CB1	4675668CDI	153825.1	403484.2c	1459432CB1	1459432CD1	1096583.1	516300CB1	516300CD1	627856CB1	627856CD1	1823159CB1	1823159CD1	232567.4	218419.1	1630551CB1	1630551CD1	360961.19	809809CB1	809809CD1	2558815CB1	2558815CD1	242010.16	1678695CB1	1678695CD1	988653.1	1250434CB1	1250434CD1	236196.3	442308.1

TOGAGUES "UZZESA

Incyle Unique	0 Human mRNA for cathepsin C.	0 Human mRNA for cathepsin C.	2.00E-75 Rat brain mRNA for sodium channel protein I.	Incyte Unique	Incyte Unique	Incyte Unique	Incyte Unique	0 Human B61 mRNA, complete cds.	0 Human B61 mRNA, complete cds.	0 Human mRNA for IFN-inducible gamma2 protein.	0 Human mRNA for IFN-inducible gamma2 protein.	0 Human leukemia virus receptor 1 (GLVR1) mRNA, complete eds.	0 Human leukemia virus receptor 1 (GLVR1) mRNA, complete cds.	0 Human vascular endothelial growth factor mRNA, complete cds.	0 Human hbc647 mRNA sequence.	Incyte Unique	3.50E-17 serine protease inhibitor	0 Human CD53 glycoprotein mRNA, complete cds.	0 Human mRNA for HM145.	0 Human cAMP response element regulatory protein (CREB2) mRNA, complete cds.	0 Human mRNA for DNA binding protein TAXREB67.	0 Human KIAA0417 mRNA, complete cds.	0 Human peroxisomal D3,D2-enoyl-CoA isomerase (PECI) mRNA, complete cds.	0 Human mRNA for KIAA0201 gene, complete cds.	0 Human heat shock protein, E. coli DnaJ homologue mRNA, complete cds.	0 Human heat shock protein, E. coli DnaJ homologue mRNA, complete cds.	0 Human odc1 mRNA for ornithine decarboxylase.	0 Human odc1 mRNA for ornithine decarboxylase.	2.00E-34 Human CC chemokine gene cluster, complete sequence.	0 Human HSPC336 mRNA, partial cds.	0 Human S100 protein beta-subunit gene, exon 3.	0 Human \$100 protein beta-subunit gene, exon 3.	0 Human protein kinase-related oncogene (PIM1) mRNA, complete cds.	0 Human c-jun proto oncogene (JUN), complete cds, clone hCl-1.	0 Human c-jun proto oncogene (JUN), complete cds, clone hCJ-1.	0 Human phosphoenolpyruvate carboxykinase (PCK1) gene, complete cds with repeats.	0 Human (clone lamda-hPEC-3) phosphoenolpyruvate carboxykinase (PCK 1) mKIVA, complete cds.
	01006656	g1006656	g57216					g179320	g179320	g30820	g30820	g306769	g306769	g3719220	g1546096		g4529920	g180142	g219862	g181040	g220087	g2887408	g4929830	g1503985	g306713	g306713	g35135	g35135	g3719360	g6841321	g337728	g337728	g1066790	g186624	g186624	g307332	g189944
060957.1	014284CB1	014284CD1	1095192.1	233003.20	1911808CB1	1911808CD1	978276.8	405844.21	405844.22	2705515CB1	2705515CD1	2023119CB1	2023119CD1	1000084.27	220134.1	216331.1	206044.1	382906.16	331306.1	1094829.20	1094829.38	1135580.4	196623.3	048488.32	2767012CB1	2767012CD1	1651724CB1	1651724CD1	206397.1	461707.40	2706645CB1	2706645CD1	474372.7	3592543CB1	3592543CD1	048612.12c	048612.13
152	153	154	155	156	157	158	159	160	191	162	163	164	165	991	167	891	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189

rograda - nyarra

 0 Human rhoB gene mRNA. 0 Human mRNA for TGF-beta superfamily protein, complete cds. 5.00E-94 Human mRNA for cytoskeletal gamma-actin. 0 Human metallothionein I-B gene, exon 3. 0 Human mRNA for Drg1 protein. 0 Human mRNA for Drg1 protein. 	Incyte Unique Incyte Unique Incyte Unique Incyte Unique Incyte Unique 0 Human cysteine-rich heart protein (hCRHP) mRNA, complete cds. 0 Human heat-shock protein HSP70B' gene. 0 Human heat-shock protein HSP70B' gene. 0 Human heat-shock protein HSP70B' gene. 0 Human ntymosin beta 10 mRNA, complete cds. 0 Human mRNA for ribosomal protein S26. 0 Human mRNA for ribosomal protein S26. 0 Human mRNA for ribosomal protein S26. 0 Human mRNA; cDNA DKFZp434F205 (from clone DKFZp434F205); complete cds. 0 Human mRNA; cDNA DKFZp434F205 (from clone DKFZp434F205); complete cds.	0 Human mRNA; cDNA DKF2p434F2D3 (from clone DKF2p434F2D3); complete cds. Incyte Unique 0 Human pRGR1 mRNA, partial cds. 7.00E-77 Human HepG2 3' region Mbol cDNA, clone hmd2d06m3. 2.00E-09 Human HepG2 partial cDNA, clone hmd2d06m5. 0 Human Id3 gene for HLH type transcription factor. 0 Human RNA for MTP. 0 Human iver glucose transporter-like protein (GLUT2), complete cds. 0 Human secretory protein (P1.B) mRNA, complete cds. 0 Human secretory protein (P1.B) mRNA, complete cds. 0 Human collagenase and stromelysin genes, complete cds. 0 Human mRNA for 90-kDa heat-shock protein. 0 Human mRNA for puromycin sensitive aminopeptidase, partial. 0 Human mRNA for puromycin sensitive aminopeptidase, partial. 0 Human mRNA for KIAA0287 gene, partial cds. 6.00E-11 Human pex3 gene (joined cds, promoter and exon 1). 6.00E-11 Human pex3 gene (joined cds, promoter and exon 1). Incyte Unique 0 Human amphiregulin (AR) mRNA, complete cds, clones lambda-AR1 and lambda-AR2.
g36031 g1813326 g1813326 g28338 g188709 g2344811 g2344811	g719268 g719268 g35221 g35221 g39660 g296451 g6807670	g6807670 g6594626 g598640 g313212 g469095 g187133 g402482 g1688257 g3287488 g3287488 g32487 g4210725 g4210725 g4218425
245259.16 522433CB1 522433CD1 1040667.43 2048551CB1 2048551CD1 1969731CB1	1220743CB1 2120743CB1 2120743CD1 3551330CB1 1440032CB1 1440032CD1 1000133.1 4020439CB1 2507087CB1 2507087CB1	2507087CDI 239996.1 1097380.1 021524.9 253987.16 344553.1 410785.1 237623.6 076047.1 1099500.15 1099500.18 2278688CBI 2278688CBI 2278688CBI 330283.1 1720847CBI 1720847CBI 1720847CBI
190 191 192 193 194 196 197	200 200 201 202 203 204 205 206 209	209 210 211 212 213 214 214 217 218 219 220 220 221 222 223 224 225

nograpia in the contract of th

g179039 0 Human amphiregulin (AR) mRNA, complete cds, clones lambda-AR1 and lambda-AR2.			g2546963 0 Human mRNA for diubiquitin.					g5912019 0 Human mRNA; cDNA DKFZp434H0735 (from clone DKFZp434H0735); partial cds.	Incyte Unique	g186757 0 Human protein kinase mRNA.	g927597 0 Human transcription factor TFIIIB 90 kDa subunit (hTFIIIB90) mRNA, complete cds.	g3005586 0 Human Ser/Arg-related nuclear matrix protein (SRM160) mRNA, complete cds.	g187109 0 Human 14 kd lectin mRNA, complete cds.	g187109 0 Human 14 kd lectin mRNA, complete cds.	3.00E-1	0			g178848 0 Human apolipoprotein E mRNA, complete cds.	g28771 0 Human mRNA for apolipoprotein AI (apo AI)=.	g28771 0 Human mRNA for apolipoprotein AI (apo AI)=.	g763428 0 Human mRNA clone with similarity to L-glycerol-3-phosphate:NAD oxidoreductase and albumin gene se	g2072161 0 Human tubby related protein 1 (TULP1) mRNA, complete cds.	g682747 0 Human mRNA for Apo1_Human (MER5(Aop1-Mouse)-like protein), complete cds.	Incyte Unique	g6466185 0 Human zinc finger protein ZNF228 (ZNF228) mRNA, complete cds.	817 0.1	g2921872 0 Human spleen mitotic checkpoint BUB3 (BUB3) mRNA, complete cds.	Incyte Unique	Incyte Unique		1 91	489 1.00E-8	g6841489 0 Human HSPC134 mRNA, complete cds.		g3978170 4.00E-36 Mus musculus lysyl oxidase-related protein 2 (Lor2) mRNA,	g2661055 6.00E-25 Human clone 23863 mRNA, partial cds.
g17903	8689g	g66300	g25469	g25469	g54167	g27083	g27083	g59120		g18675	g92759	g30055	g18710	g18710	g42402	g39548	g39548	g17884	g17884	g28771	g28771	g76342	g20721	g68274		g64661	g73398	g29218			g11434	g11434	g68414	g68414		g39781	g2661(
3478236CD1	147541.17	331120.16c	575983CB1	575983CD1	413268.6	1989186CB1	1989186CD1	337448.1c	228304.19	420527.25	998034.3	474165.26	697785CB1	697785CD1	346209.3	167772CB1	167772CD1	2514988CB1	2514988CD1	481231.16	481231.17	1045853.2	336615.1	1328423.2	085282.1	1081605.3	1053517.1	480169.76	2636043CB1	2636043CD1	2993696CB1	2993696CD1	240518.21	240518.34	001322.4c	350502.3	350502.4c
228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265

TABLE 3

	6.40E-43 hypothetical protein	0 Human DNA-binding protein (Fil-1) gene, 5' end of cds.	0 Human epidermal growth factor receptor (HER3) mRNA, complete cds.	0 Human clone 23929 mRNA sequence.	0 Human clone 23929 mRNA sequence.	0 Human metallothionein (MT)I-F gene, complete cds.	0 Human metallothionein (MT)I-F gene, complete cds.	3.00E-36 Human guanine nucleotide-binding protein alpha-subunit gene (G-s-alpha), exon 2.	0 Human HK2 mRNA for hexokinase II.	0 Human HK2 mRNA for hexokinase II.	Incyte Unique	0 Human mRNA for PTB-associated splicing factor.	0 Human mRNA for PTB-associated splicing factor.	0 Human mRNA for KIAA0343 gene, complete cds.	0 Human phosphoglycerate mutase 2 (muscle specific isozyme) (PGAM2) gene, 5' end.	0 Human mRNA for exportin (tRNA).	0 Human mRNA for exportin (tRNA).	0 Human MEM-102 glycoprotein mRNA, complete cds.	0 Human mRNA for RNF3A (DONG1) ring finger protein.	0 Human mRNA for RNF3A (DONG1) ring finger protein.	0 Human gene for JKTBP2, JKTBP1, complete cds.	0 Human mRNA for BiP protein.	0 Human mRNA for KIAA0647 protein, partial cds.	4.00E-28 Human mRNA for U61 small nuclear RNA.	0 Human thymosin beta 10 mRNA, complete cds.	0 Human thymosin beta 10 mRNA, complete eds.	0 thymosin beta-10 [Human, metastatic melanoma cell line, mRNA, 453 nt].	5.00E-23 Human genomic DNA, chromosome 22q11.2, clone KB1561E1.	1.00E-13 IL-17 receptor [Homo sapiens]	0 Human mRNA for hBD-1 protein.	0 Human mRNA for hBD-1 protein.	0 Human IgE-binding protein (epsilon-BP) mRNA, complete cds.	0 Human IgE-binding protein (epsilon-BP) mRNA, complete cds.	0 Human (clone lamda-hPEC-3) phosphoenolpyruvate carboxykinase (PCK1) mRNA, complete cds.	0 Human (clone lamda-hPEC-3) phosphoenolpyruvate carboxykinase (PCK1) mRNA, complete cds.	Incyte Unique	Incyte Unique	Rattus norvegicus mRNA for atypical PKC specific binding
	g2664429	g1000863	g183990	g3360429	g3360429	g187542	g187542	g183398	g587201	g587201		g38457	g38457	g2224626	g189869	g2924334	g2924334	g187518	g2437832	g2437832	g4512253	g1143491	g3327107	g1321847	g339660	g339660	g264772	g6016843	g2826476	g1617087	g1617087	g179530	g179530	g189944	g189944			g3868777
	253783.3	085119.1	902559.1	4113161CB1	4113161CD1	2757583CB1	2757583CD1	198317.1	1508254CB1	1508254CD1	474691.3	2457215CB1	2457215CD1	201395.4c	233189.21	196606.6c	196606.8c	1040190.3	1427459CB1	1427459CD1	480453.16c	1095604.1	241291.28	230611.1	3993708CB1	3993708CD1	1000133.12	400253.17c	400253.5	030882CB1	030882CD1	898779CB1	898779CD1	3727408CB1	3727408CD1	984236.1c	984236.2c	348082.5
ì	506	267	268	569	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303

THE TENT OF THE PRINT

TABLE 3

0 atypical PKC specific binding protein [Rattus norvegicus] 0 Human cytochrome P1-450 (TCDD-inducible) mRNA, complete cds. 0 Human mRNA; cDNA DKFZp566M0947 (from clone DKFZp566M0947). 4.00E-56 Human minisatellite ceb1 repeat region. Incyte Unique Incyte Unique Homo sapiens FK506 binding protein precursor (FKBP22) Incyte Unique	 0 Human pre-mRNA splicing factor (SFRS3) mRNA, complete cds. 0 Human pre-mRNA splicing factor (SFRS3) mRNA, complete cds. 0 Human pre-mRNA splicing factor (SFRS3) mRNA, complete cds. 0 Human vacuolar H(+)-ATPase subunit mRNA, complete cds. 0 Human GAP SH3 binding protein mRNA, complete cds. 0 Human GAP SH3 binding protein mRNA, complete cds. 0 Human mRNA for slow skeletal troponin C (TnC). 0 Human mRNA for slow skeletal troponin C (TnC). 0 Human scrinc-threonine kinase (BTAK) gene, partial cds. 0 TI S=translocated in linosarcoma [Human, mRNA, 1824 nt]. 	0 TLS/CHOP=hybrid gene {translocation breakpoint} [Human, myxoid liposarcomas cells, mRNA Mutant, 0 TLS/CHOP=hybrid gene {translocation breakpoint} [Human, myxoid liposarcomas cells, mRNA Mutant, 0 Human polyadenylate binding protein (TIA-1) mRNA, complete cds. Incyte Unique 2.00E-14 Human 88-kDa Golgi protein (GM88) mRNA, complete cds. 2.8 35 kDa protein [Bartonella henselae] Incyte Unique Incyte Unique Incyte Unique	 0 Human ferritin L chain mRNA, complete cds. 0 Human nerritin L chain mRNA, complete cds. 0 Human NAP (nucleosome assembly protein) mRNA, complete cds. 0 Human mRNA for KIAA0695 protein, complete cds. 1 Incyte Unique 0 Human glutamate dehydrogenase (GDH) mRNA, complete cds. Incyte Unique 0 Human mRNA for KIAA0914 protein, complete cds. 0 Human fibroblast mRNA for aldolase A.
g3868778 g181275 g6453594 g2935483	g5531903 g5531903 g5531903 g3329377 g1051169 g1051169 g37207 g37207	g386158 g339700 g6808610 g710405	g182513 g182513 g189066 g3327203 g3327203 g183059 g4240316
348082.7 1097910.1 246841.1 351241.1 2790762CB1 2790762CD1 2253717CB1	2655184CB1 2655184CB1 363000.9c 232818.15 347781.10 2477616CB1 2477616CD1 360532.1 360532.9 110245.1 478620 53	181344CB1 1813444CD1 474588.21 407838.1 994387.19 347796.7 406498.4c 3346307CB1	4005778CB1 4005778CD1 995575.17 863406CB1 863406CD1 413864.17 350106.16 399785.1 010498.19
304 305 306 307 308 310	312 313 314 315 316 318 320 320	323 324 325 325 326 327 330 331	332 334 335 336 337 339 340

TABLE 3

0 Human aldolase A mRNA, complete cds. 0 Human aldolase A mRNA, complete cds.	5.00E-86 Human gonadotropin releasing hormone receptor (GNKHK) gene, exon 1. 0 Human mRNA for cytoskeletal gamma-actin.	0 Human cysteine protease CPP32 isoform alpha mRNA, complete cds.	Incyte Unique	Incyte Unique	Incyte Unique	0 Human mRNA for transferrin receptor.	0 Human mRNA for histidase, complete cds.	0 Human mRNA for enteric smooth muscle gamma-actin.	Incyte Unique	Incyte Unique		5.00E-2	0 Human X104 mRNA, complete cds.	0 Human X104 mRNA, complete cds.	0 Human follistatin-related protein precursor mRNA, complete cds.			0 Human myosin-IXb mRNA, complete cds.	Incyte Unique	Incyte Unique	Incyte Unique	0 Human mRNA for voltage-activated sodium channel.	0 Human mRNA for voltage-activated sodium channel.	6.00E-64 Human EMX1 mRNA.	0 Human mRNA clone with similarity to L-glycerol-3-phosphate:NAD oxidoreductase and albumin gene sc	0 Human mRNA clone with similarity to L-glycerol-3-phosphate:NAD oxidoreductase and albumin gene se	0.08						0 Human pephBGT-1 betaine-GABA transporter mRNA, complete cds.	0 Human pephBGT-1 betaine-GABA transporter mRNA, complete cds.	0 Human mRNA for tyrosine aminotransferase (TAT) (EC. 2.0.1.3).
g178350 g178350	g2290764 g28338	g561665				g37432	g451209	g36502			g456587	g5360203	g498012	g498012	g536897	g536897	g5262490	g1147782				g758109	g758109	g31139	g763428	g763428	g2769702	g1017792	g28335	g4240476	g5102577	g5926690	g881474	g881474	g36712
2706606CB1 2706606CD1	118006.1 1039889.26	481480.7	662575CB1	662575CD1	027619.3	235447.5	331104.2	348390.2	127004.1	026190.1	250330.1	480375.28	364726.10	364726.12	1505038CB1	1505038CD1	903508.12	346716.17c	346716.21c	330776.1	407999.1c	1719478CB1	1719478CD1	351157.2	088957CB1	088957CD1	980446.1	198827.1	1102297.22	215112.1	171495.1	242010.43	5834958CB1	5834958CD1	335648.1c
342 343	344 345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379

DGG19UBG ...UFEDG1

TABLE 3

13 0 Human glucose-6-phosphatase mRNA, complete cds. 10 9 0 Human homeobox protein MEIS2 (MEIS2) mRNA, partial cds. 18 5 00E 13 Human Aladra NA		060 0 Human cytoplasmic dynein light chain 1 (hdlc1) mRNA, complete cds.	o Human ribonucleoprotein (La) mRNA, 3' end.	36 0 Human La protein mRNA, complete cds.	5 0 Human hsc70 gene for 71 kd heat shock cognate protein.	33 0 African green monkey hsp70 mRNA.	96 0 Human thyroxine-binding globulin mRNA, complete cds.	96 0 Human thyroxine-binding globulin mRNA, complete cds.	503 0 Human dickkopf-1 (DKK-1) mRNA, complete cds.	99 0 Human mRNA for lipocortin II, complete cds.	99 0 Human mRNA for lipocortin II, complete cds.	l 0 Human urf-ret mRNA.	2.00E-36 Rattus norvegicus developmentally regulated protein mRNA,	Incyte Unique	Incyte Unique	3.00E-49 Human 7SK RNA gene and flanking regions.	3.		1.00E-12 Human connective tissue growth factor related protein WISP-2 (WISP2) mRNA, complete cds.
g452443 g2394309	817471	g1209060	g337456	g178686	g32466	g313283	g338696	g338696	g6049603	g219909	g219909	g37611	g310099			g23915	g2342725	g1021027	g4028582
333840.1 480885.2 008106.85	400701.4	1100320.4	246727.11	246727.17	1102322.12c	1102322.18	2070610CB1	2070610CD1	336733.3	1326902.13	1326902.6	013521.16	985369.1	002455.1	372647.1	208075.1	209279.1	381058.1	046977.1

Lugarda Carobota TABLE 4

1 220060.4 6 3201389CD 8 086390CD1 9 1102322.16 11 1545176CD 12 978222.4 15 1720920CD 17 1857017CD 19 2114865CD 21 2700132CD 22 238349.2 27 2516070CD 29 167507CD1 31 3860413CD 33 3393861CD 34 030850.7 40 1269631CD 40 1269631CD 47 476301CD1 54 978740.3 54 978740.3 56 348072.5 66 3603037CD 66 085596CD1 66 085596CD1 66 085596CD1		STOP	FRAME	Pfam ID	Pfam Description	E-value
E O 2 2 - 2 - 2 - 2 - 2 - 2 4 - 2 - 2	4	441	forward 1	Transthyretin	Transthyretin precursor (formerly prealbumin)	8.20E-103
0 6 6 - 6 - 6 - 6 - 6 - 6 - 6 -	CD1 43	326		7tm_1	7 transmembrane receptor (rhodopsin family)	4.20E-103
	3D1 21	130		SAA_proteins	SAA_proteins Serum amyloid A protein	3.00E-85
	3.16	803	forward 3	HSP70	Hsp70 protein	2.40E-12
9 4 4 4 4 - E E 4 9 4 6 6 4 E 9 E 9 4	(CD1 6	612		HSP70	Hsp70 protein	0.00E+00
	-	159	forward 1	НГН	Helix-loop-helix DNA-binding domain	1.10E-10
	CD1 55	181		laminin_G	Laminin G domain	2.00E-25
2 2 3 3 1 6 6 7 5 1 1 1 4 6 6 7 6 5 6 7	CD1 475	871		HMG-CoA_re	HMG-CoA_re Hydroxymethylglutaryl-coenzyme A reductase	1.10E-298
2 4 4 - 6 6 4 6 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	CD1 46	420		serpin	Serpins (serine protease inhibitors)	1.60E-216
4 4 1 6 6 7 6 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	CD1 27	16		FHA	FHA domain	4.30E-21
2 - 6 6 7 5 - 1 - 1 - 4 6 6 7 6 5 5 6	2 379	837	forward 1	SCP	SCP-like extracellular protein	1.40E-34
	(CD) 2	265		Apolipoproteir	Apolipoproteir Apolipoprotein A1/A4/E family	2.00E-137
E E C O C C C C C C C C C C C C C C C C	3D1 266	370		cystatin	Cystatin domain	3.40E-39
6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	CDI	19		metalthio	Metallothionein	2.10E-25
2 2 1 1 1 4 6 6 2 6 6 0 6 0 4	CDI 234	484		fibrinogen_C	Fibrinogen beta and gamma chains, C-terminal globular domain	3.00E-179
0 1 1 4 6 6 7 6 0 6 0 4	CD1 38	183		lipocalin	Lipocalin / cytosolic fatty-acid binding protein family	2.10E-33
1 4 6 6 6 6 6 6 6 6 6	7	396	forward 1	arf	ADP-ribosylation factor family	1.30E-05
4000000	CD1 1651	1735		En3	Fibronectin type III domain	9.40E-10
	_	1237		ldl_recept_a	Low-density lipoprotein receptor domain class A	2.50E-17
		931		ldl_recept_b	Low-density lipoprotein receptor repeat class B	2.00E-06
	3D1 28	286		transketolase	Transketolase	7.20E-124
		1487	forward 3	PH	PH domain	5.10E-06
		1049	forward 3	RhoGEF	RhoGEF domain	1.10E-23
	_	585		Noll_Nop2_S	NoII_Nop2_S NOLI/NOP2/sun family	2.80E-157
• • • • •	998 5	1411	forward 2	vwa	von Willebrand factor type A domain	8.80E-13
	ZD1 17	126		cystatin	Cystatin domain	3.10E-25
- ,	CD1 340	364		zf-C2H2	Zinc finger, C2H2 type	5.50E-07
	,D1 24	68		IL8	Small cytokines (intecrine/chemokine), interleukin-8 like	2.50E-10
	2 1111	1953	forward 1	pyr_redox	Pyridine nucleotide-disulphide oxidoreductase class-I	7.60E-05
70 407096.2		1489	forward 2	pyr_redox	Pyridine nucleotide-disulphide oxidoreductase class-1	3.20E-06
70 407096.2	2 786	1730	forward 3	pyr_redox	Pyridine nucleotide-disulphide oxidoreductase class-I	1.70E-09
71 209265.54	54 2041	2250	forward 1	SH3	SH3 domain	1.30E-05
73 701484CDI	;D1 8	614		HSP70	Hsp70 protein	0.00E+00
74 251859.2	2 348	632	forward 3	FKBP	FKBP-type peptidyl-prolyl cis-trans isomerases	9.40E-49
76 3766715CD	CD1 170	198		TPR	TPR Domain	7.70E-04
83 1434821CD	CD1 30	71		trefoil	Trefoil (P-type) domain	1.00E-24

LANDER OF THE TRANSPORT OF THE PROPERTY OF THE

84	289671.27	1273	1614	forward 1	GSHPx	Glutathione peroxidases	4.40E-68
98	1282225CD1	2	127		lipocalin	Lipocalin / cytosolic fatty-acid binding protein family	6.90E-25
83	263336.57	55	171	forward I	metalthio	Metallothionein	8.20E-06
88	464689.40	443	631	forward 2	cystatin	Cystatin domain	6.90E-21
16	243794.23	270	434	forward 3	Ribosomal_S	Ribosomal_S1 Ribosomal protein S14p/S29e	6.80E-19
86	347055.4	279	1649	forward 3	HMG_CoA_s	HMG_CoA_s; Hydroxymethylglutaryl-coenzyme A synthase	0.00E+00
66	898899.11	199	1266	forward 1	trypsin	Trypsin	2.10E-39
66	898899.11	281	517	forward 2	kringle	Kringle domain	1.50E-50
901	898899.32	1222	1383	forward 1	kringle	Kringle domain	5.60E-09
901	898899.32	379	609	forward 1	PAN	PAN domain	1.50E-06
100	898899.32	1367	1543	forward 2	kringle	Kringle domain	1.10E-07
8	898899.32	2141	2785	forward 2	trypsin	Trypsin	4.50E-46
901	898899.32	723	965	forward 3	kringle	Kringle domain	1.40E-21
102	2047630CDI	206	557		Asn_synthase	Asparagine synthase	9.00E-261
102	2047630CD1	2	148		GATase_2	Glutamine amidotransferases class-II	9.90E-65
103	1039889.8	265	1002	forward 1	actin	Actin	2.40E-83
103	1039889.8	896	1204	forward 2	actin	Actin	5.30E-43
103	1039889.8	1281	1694	forward 3	actin	Actin	4.40E-67
105	1272969CDI	62	391		filament	Intermediate filament proteins	4.30E-157
109	1448817CD1	30	68		IGFBP	Insulin-like growth factor binding proteins	2.20E-23
109	1448817CD1	176	251		thyroglobulin_	. Thyroglobulin type-1 repeat	5.50E-40
011	1100769.2	262	603	forward 1	Ribosomal_S2	Ribosomal_S2 Ribosomal protein S26e	9.20E-75
011	1100769.2	699	884	forward 3	Ribosomal_S2	Ribosomal_S2 Ribosomal protein S26e	9.80E-30
112	225080.16	510	641	forward 3	prenyltrans	Prenyltransferase and squalene oxidase repeat	6.50E-13
113	334851.5	138	452	forward 3	СН	Calponin homology (CH) domain	2.00E-25
114	995529.7	46	726	forward 1	pkinase	Eukaryotic protein kinase domain	6.00E-46
115	995529.8	53	992	forward 2	pkinase	Eukaryotic protein kinase domain	1.00E-87
115	995529.8	795	872	forward 3	pkinase	Eukaryotic protein kinase domain	2.70E-07
911	201851.1	1634	1750	forward 2	WD40	WD domain, G-beta repeat	1.20E-08
811	059509CDI	153	280		TNF	TNF(Tumor Necrosis Factor) family	4.00E-15
611	481231.14	112	573	forward 1	Apolipoprotei	Apolipoproteir Apolipoprotein A1/A4/E family	5.80E-34
124	153825.1	820	951	forward 1	hemopexin	Hemopexin	3.80E-14
124	153825.1	42	497	forward 3	Peptidase_M11 Matrixin	Matrixin	5.70E-13
127	1459432CD1	27	311		7tm_1	7 transmembrane receptor (rhodopsin family)	2.30E-64
130	516300CD1	87	174		lectin_c	Lectin C-type domain	7.50E-05
132	627856CD1	143	239		tRNA_bind	Putative tRNA binding domain	5.80E-46
135	232567.4	305	1042	forward 2	kazal	Kazal-type serine protease inhibitor domain	2.30E-17
139	360961.19	1186	1266	forward 1	S-AdoMet_sy	S-AdoMet_syr S-adenosylmethionine synthetase	1.80E-22

Future of the second

4 00E-87	(0 E)0:: 90 E)0E	3.50E-216	0.00E+00	0.00E+00	1.00E-06	1.60E-10	2.70E-27	8.30E-106	7.60E-80	1.30E-96	1.10E-37	2.90E-30	0.00E+00	2.40E-279	7.10E-25	4.40E-04	8.90E-08	2.50E-88	2.90E-19	2.90E-19	3.80E-06	6.10E-40	2.70E-220	1.40E-34	2.50E-07	5.80E-43	2.30E-202	5.90E-06	3.60E-23	3.80E-88	4.90E-22	0.00E+00	6.90E-91	6.80E-19	1.80E-24	9.50E-15
S-AdoMet syt S-adenosylmethionine synthetase	Zinc finger C3HC4 type (RING finger)	Aldehyde dehydrogenase family	Hsp70 protein	Hsp70 protein	Zinc finger, C2H2 type	PAC motif	Homeobox domain	Papain family cysteine protease	Ephrin	Ephrin	RNA-synt_1btRNA synthetases class I (W and Y)	WHEP-TRS domain containing proteins	Phosphate transporter family	Tubulin/FtsZ family	Serpins (serine protease inhibitors)	transmembran Transmembrane 4 family	7 transmembrane receptor (rhodopsin family)	7 transmembrane receptor (rhodopsin family)	bZIP transcription factor	bZIP transcription factor	Enoyl-CoA hydratase/isomerase family	Acyl CoA binding protein	Hsp70 protein	DnaJ domain	DnaJ C terminal region	DnaJ_CXXCX DnaJ central domain (4 repcats)	Orn_DAP_Arg Pyridoxal-dependent decarboxylase	EF hand	S-100/ICaBP type calcium binding domain	Eukaryotic protein kinase domain	bZIP transcription factor	Phosphoenolpyruvate carboxykinase	Ras family	Transforming growth factor beta like domain	Metallothionein	Transmembrane amino acid transporter protein
S-AdoMet sv	zf-C3HC4	aldedh	HSP70	HSP70	zf-C2H2	PAC	homeobox	Peptidase_C1	Ephrin	Ephrin	tRNA-synt_1	WHEP-TRS	PHO4	tubulin	serpin	transmembrar	7tm_1	7tm_1	bZIP	bZIP	ЕСН	ACBP	HSP70	DnaJ	DnaJ_C	DnaJ_CXXC	Orn_DAP_Ar	efhand	S_100	pkinase	6ZIP	PEPCK	ras	TGF-beta	metalthio	Aa_trans
forward 2			forward 1		forward 2		forward 3		forward I	forward 1				forward 2	forward 2	forward 2	forward 1	forward 3	forward 3	forward 3	forward 1	forward 3	forward 3							forward 1		forward 2	forward 2			forward 2
604	303	511	2037	612	1369	346	464	458	498	573	381	89	999	1423	532	226	1029	1001	1559	1886	984	413	2465	89	346	207	400	8	47	1164	314	1984	955	308	61	1768
149	264	45	217	9	1295	303	294	231	133	157	158	12	39	152	248	182	296	312	1365	1692	511	159	348	9	220	121	40	53	4	406	250	203	398	211	_	518
360961.19	809809CD1	2558815CD1	242010.16	1678695CD1	988653.1	1250434CD1	442308.1	014284CD1	405844.21	405844.22	2705515CD1	2705515CD1	2023119CD1	1000084.27	206044.1	382906.16	331306.1	331306.1	1094829.20	1094829.38	196623.3	196623.3	048488.32	2767012CD1	2767012CD1	2767012CD1	1651724CD1	2706645CD1	2706645CD1	474372.7	3592543CDI	048612.13	245259.16	522433CD1	2048551CD1	1326983.14
139	141	143	144	146	147	149	151	154	160	191	163	163	165	166	169	170	171	171	172	173	175	175	176	178	178	178	180	184	184	185	187	189	190	192	195	198

202	3551330CD1	4	19		LIM	LIM domain containing proteins	2.10E-19
204	1440032CD1	œ	614		HSP70	Hsp70 protein	0.00E+00
205	1000133.1	199	321	forward 1	Thymosin	Thymosin beta-4 family	1.90E-21
207	4020439CD1	_	114		Ribosomal_S2	Ribosomal_S2 Ribosomal protein S26e	4.70E-67
213	021524.9	318	434	forward 3	WD40	WD domain, G-beta repeat	1.80E-06
215	344553.1	159	1820	forward 3	Vitellogenin_	Vitellogenin_L Lipoprotein amino terminal region	1.80E-160
216	410785.1	72	1535	forward 3	sugar_tr	Sugar (and other) transporter	2.40E-200
217	237623.6	155	280	forward 2	trefoil	Trefoil (P-type) domain	2.00E-25
219	1099500.15	466	1116	forward 1	HSP90	Hsp90 protein	1.20E-128
219	1099500.15	263	472	forward 2	HSP90	Hsp90 protein	5.50E-41
219	1099500.15	102	287	forward 3	HSP90	Hsp90 protein	1.00E-41
220	1099500.18	1187	1630	forward 2	HSP90	Hsp90 protein	1.70E-113
220	1099500.18	480	2609	forward 3	HSP90	Hsp90 protein	0.00E+00
222	2278688CD1	54	<u>4</u>		Peptidase_M1	Peptidase family M1	2.90E-234
223	380283.1	Ξ	392	forward 3	SCAN	SCAN domain	2.80E-11
223	380283.1	2889	2957	forward 3	zf-C2H2	Zinc finger, C2H2 type	3.20E-06
232	575983CD1	œ	79		ubiquitin	Ubiquitin family	7.90E-09
235	1989186CD1	447	752		HECT	HECT-domain (ubiquitin-transferase).	5.70E-130
235	1989186CD1	586	318		ww	WW domain	3.00E-16
238	420527.25	924	1871	forward 3	pkinase	Eukaryotic protein kinase domain	5.90E-79
239	998034.3	931	1152	forward I	transcript_fac2	transcript_fac2 Transcription factor TFIIB repeat	5.80E-19
240	474165.26	244	465	forward 1	PWI	PWI domain	2.60E-41
242	697785CD1	22	126		Gal-bind_lecti	Gal-bind_lecti Vertebrate galactoside-binding lectins	2.90E-65
243	346209.3	285	2861	forward 3	Myosin_tail	Myosin tail	2.00E-181
245	167772CD1	_	61		metalthio	Metallothionein	2.20E-23
247	2514988CD1	7	284		Apolipoproteir	Apolipoproteir Apolipoprotein A1/A4/E family	9.20E-144
248	481231.16	11	823	forward 2	Apolipoproteir	Apolipoproteir Apolipoprotein A1/A4/E family	2.90E-123
249	481231.17	829	1599	forward 1	Apolipoprotein	Apolipoproteir Apolipoprotein A1/A4/E family	2.20E-130
249	481231.17	216	986	forward 3	Apolipoproteir	Apolipoproteir Apolipoprotein A1/A4/E family	1.60E-103
250	1045853.2	955	1713	forward 1	NAD_Gly3P_0	NAD_Gly3P_(NAD-dependent glycerol-3-phosphate dehydrogenase	2.00E-11
250	1045853.2	1889	2413	forward 2	transport_prot	transport_prot Serum albumin family	1.20E-89
251	336615.1	98	874	forward 2	Tub	Tub family	3.00E-195
254	1081605.3	177	365	forward 3	KRAB	KRAB box	4.10E-29
254	1081605.3	2649	2717	forward 3	zf-C2H2	Zinc finger, C2H2 type	3.90E-08
256	480169.76	337	453	forward I	WD40	WD domain, G-beta repeat	2.80E-07
260	2993696CD1	30	989		HSP70	Hsp70 protein	0.00E+00
566	253783.3	926	1185	forward 1	rrm	RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	6.40E-21
566	253783.3	926	1185	forward 1	rrm	RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	6.40E-21

1.70E-97	6 50F-60	3.20E-61	1.20E-24	0.00E+00	8.40E-16	5.60E-14	9.30E-21	1.80E-24	1.80E-24	3.80E-50	1.20E-19	4.60E-107	1.40E-27	5.30E-67	1.70E-12	3,00E-08	3.00E-08	1.10E-17	1.50E-11	9.20E-21	6.90E-09	6.90E-99	8.80E-191	2.50E-234	2.30E-07	1.70E-200	9.60E-192	2.70E-65	7.60E-270	3.90E-190	2.40E-89	6.40E-41	0.00E+00	9.40E-59	7.10E-17	5.60E-10	9.20E-20
Furin-like cysteine rich region	Becen I dom Becentor I domain	Eukarvotic protein kinase domain	Metallothionein	Hexokinase	RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	Zinc finger, C3HC4 type (RING finger)	FYVE zinc finger	Thymosin beta-4 family	Thymosin beta-4 family	i Vertebrate galactoside-binding lectins	PDZ domain (Also known as DHR or GLGF).	Cytochrome P450	FKBP-type peptidyl-prolyl cis-trans isomerases	Nuclear transport factor 2 (NTF2) domain	RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	EF hand	EF hand	RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	Zn-finger in Ran binding protein and others.	RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	Ferritins	Nucleosome assembly protein (NAP)	Cullin family	Ank repeat	GLFV_dchydr Glutamate/Leucine/Phenylalanine/Valine dehydrogenase	glycolytic_enz Fructose-bisphosphate aldolase class-I	glycolytic_enz Fructose-bisphosphate aldolase class-I	glycolytic_enz Fructose-bisphosphate aldolase class-I	Actin	Actin	ICE-like protease (caspase) p10 domain	Phenylalanine and histidine ammonia-lyases	Actin	Guanylate_kin Guanylate kinase	Guanylate_kin Guanylate kinase	PDZ domain (Also known as DHR or GLGF).
Furin-like	Recen I don	nkinase	metalthio	hexokinase	ırm	zf-C3HC4	FYVE	Thymosin	Thymosin	Gal-bind_lecti	PDZ	p450	FKBP	NTF2	rrm	efhand	efhand	rrm	zf-RanBP	rrm	rrm	ferritin	NAP_family	Cullin	ank	GLFV_dchyd	glycolytic_enz	glycolytic_ena	glycolytic_enz	actin	actin	ICE_p10	PAL	actin	Guanylate_kir	Guanylate_kir	PDZ
forward 1	forward 1	forward 3					forward 1		forward 1		forward 2	forward 2				forward 1	forward 2	forward 3	forward 3	forward 1	forward 3		forward 1		forward 1	forward 1	forward 1	forward 3		forward 2	forward 3	forward 1	forward 1	forward 3	forward 3	forward 1	forward 1
1191	733	2996	19	463	364	09	3267	42	198	239	946	835	141	133	402	099	529	1163	1424	2460	2075	169	1260	717	1008	1905	1317	581	364	1279	491	348	2220	413	647	2631	483
733	358	2238	-	91	566	22	3067	2	92	136	989	53	48	=	342	574	473	924	1329	2263	1863	13	439	15	016	574	899	276	15	515	1117	112	481	108	333	2317	223
902559.1	9025591	902559.1	2757583CD1	1508254CD1	2457215CD1	1427459CD1	241291.28	3993708CD1	1000133.12	898779CD1	348082.7	1097910.1	2253717CD1	2477616CD1	2477616CD1	360532.1	360532.9	478620.53	478620.53	474588.21	474588.21	4005778CD1	995575.17	863406CD1	413864.17	350106.16	255824.39	255824.39	2706606CD1	1039889.26	1039889.26	481480.7	331104.2	348390.2	364726.10	364726.12	364726.12
268	368	268	272	275	278	285	288	291	292	298	304	305	311	318	318	319	320	322	322	325	325	333	334	336	337	338	341	341	343	345	345	346	351	352	357	358	358

7.20E-12	2.00E-100	6.60E-13	1.20E-89	1.70E-286	4.10E-34	5.00E-129	0.00E+00	1.10E-62	1.00E-13	3.80E-05	2.70E-194	5.20E-18	5.20E-18	1.10E-24	1.50E-09
Kazal-type scrine protease inhibitor domain	Ion transport protein	Homeobox domain	transport_prot Serum albumin family	Actin	Homeobox domain	Hsp70 protein	Sodium:neurotransmitter symporter family	forward 3 Dynein_light Dynein light chain type 1	RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	Hsp70 protein	Serpins (serine protease inhibitors)	Annexin	Annexin	Annexin	PH domain
kazal	ion_trans	homeobox	transport_prot	actin	homeobox	HSP70	SNF	Dynein_light	шш	HSP70	serpin	annexin	annexin	annexin	PH
		forward 3 homeobox		forward 1	forward 1 homeobox	forward 2 HSP70			forward 1	forward 2 HSP70		forward 3 annexin	forward 1 annexin	forward 3	forward 3 PH
86	1445	134	202	2481	237	1267	575	503	829	751	412	473	1122	662	734
54	1177	3	28	1354	<i>L</i> 9	7	36	237	469	ĸ	39	270	616	459	486
1505038CD1	1719478CD1	351157.2	088957CD1	1102297.22	171495.1	242010.43	5834958CD1	1100320.4	246727.17	1102322.18	2070610CD1	1326902.13	1326902.6	1326902.6	013521.16
360	367	368	370	373	375	376	378	384	386	388	390	392	393	393	394

TABLE 5

SEQ ID NO:	TEMPLATE II	START	STOP	FRAME	HIT TYPE
6	3201389CD1	26	52		TM
6	3201389CD1	185	210	•	TM
6	3201389CD1	145	171		SP
9	1102322.16	127	219	forward 1	SP
9	1102322.16	313	396	forward 1	SP
12	978222.4	533	625	forward 2	SP
13	978222.5	660	737	forward 3	TM
15	1720920CD1	2220	2246		TM
15	1720920CD1	2222	2248		SP
15	1720920CD1	1	30		SP
17	1857017CD1	10	36		TM
33	3393861CD1	1	29		SP
35	2517374CD1	1	34		SP
38	237416.14	570	665	forward 3	SP
38	237416.14	863	940	forward 2	TM
40	1269631CD1	1	28	ioi waid 2	SP
50	2989375CD1	23	49		SP
54	978740.3	3103	3186	forward 1	TM
54	978740.3	652	741	forward 1	SP
55	400197.1	244	321	forward 1	TM
60	348072.5	243	323	forward 3	SP
60	348072.5	780	881	forward 3	SP
60	348072.5	132	221	forward 3	SP
60	348072.5	1659	1751	forward 3	SP
60	348072.5	10	99	forward 1	SP
68	088564CD1	1	26		SP
69	040429.1	656	739	forward 2	TM
69	040429.1	93	179	forward 3	SP
70	407096.2	1083	1157	forward 3	TM
70	407096.2	1099	1179	forward 1	SP
83	1434821CD1	1	26		SP
84	289671.27	1132	1221	forward 1	SP
84	289671.27	1298	1375	forward 2	SP
88	464689.40	281	361	forward 2	SP
89	155943.1	964	1047	forward 1	SP
89	155943.1	995	1069	forward 2	TM
95	1273641CD1	136	161		SP
98	347055.4	1769	1864	forward 2	SP
100	898899.32	242	337	forward 2	SP
109	1448817CD1	1	31		SP
111	332521.1	397	483	forward 1	SP
112	225080.16	2387	2488	forward 2	SP
114	995529.7	275	358	forward 2	SP
115	995529.8	285	368	forward 3	SP
115	995529.8	1605	1688	forward 3	TM
116	201851.1	3954	4034	forward 3	TM
118	059509CD1	3	32		SP
127	1459432CD1	41	66		TM
130	516300CD1	1	28		SP
147	988653.1	1080	1166	forward 3	SP
147	988653.1	3422	3502	forward 2	TM
150	236196.3	563	643	forward 2	TM

150	236196.3	754	834	forward 1	SP
150	236196.3	. 851	928	forward 2	TM
154	014284CD1	1	28	•	SP
159	978276.8	2041	2115	forward 1	TM
159	978276.8	2041	2115	forward 1	TM
160	405844.21	559	651	forward 1	SP
161	405844.22	649	741	forward 1	SP
165	2023119CD1	23	50		TM
165	2023119CD1	562	587		TM
166	1000084.27	4622	4705	forward 2	SP
166	1000084.27	309	410	forward 3	SP
166	1000084.27	1089	1169	forward 3	SP
166	1000084.27	4170	4259	forward 3	SP
166	1000084.27	4040	4123	forward 2	SP
166	1000084.27	4138	4227	forward 1	SP
167	220134.1	2246	2326	forward 2	TM
168	216331.1	1465	1551	forward l	TM
170	382906.16	155	238	forward 2	SP
171	331306.1	273	350	forward 3	TM
171	331306.1	2517	2594	forward 3	TM
171	331306.1	897	974	forward 3	TM
171	331306.1	576	659	forward 3	TM
172	1094829.20	1156	1242	forward 1	SP
172	1094829.20	673	756	forward l	SP
173	1094829.38	1468	1554	forward 1	SP
173	1094829.38	985	1068	forward 1	SP
174	1135580.4	4037	4120	forward 2	TM
174	1135580.4	4599	4685	forward 3	SP
174	1135580.4	4492	4581	forward 1	SP
174	1135580.4	3367	3453	forward 1	SP
174	1135580.4	1701	1790	forward 3	SP
174	1135580.4	4103	4183	forward 2	SP
175	196623.3	659	739	forward 2	SP
176	048488.32	2758	2835	forward 1	TM
182	461707.40	185	268	forward 2	SP
185	474372.7	2106	2198	forward 3	SP
185	474372.7	2084	2164	forward 2	TM
189	048612.13	663	743	forward 3	SP
192	522433CD1	1	29		SP
198	1326983.14	4115	4198	forward 2	TM
198	1326983.14	2343	2423	forward 3	TM
198	1326983.14	114	197	forward 3	TM
198	1326983.14	2467	2550	forward 1	TM
198	1326983.14	1547	1624	forward 2	TM
198	1326983.14	1406	1483	forward 2	TM
198	1326983.14	4115	4198	forward 2	TM
198	1326983.14	2343	2423	forward 3	TM
198	1326983.14	114	197	forward 3	TM
198	1326983.14	2467	2550	forward 1	TM
198	1326983.14	1547	1624	forward 2	TM
198 200	1326983.14 2120743CD1	1406 295	1483	forward 2	TM
200	2120743CD1 2120743CD1		323		TM SP
200	2120743CD1	189	219		31

•••					
200	2120743CD1	344	374		SP
200	2120743CD1	. 87	113		SP
211	1097380.1	864	962	forward 3	SP
211	1097380.1	1360	1440	forward 1	TM
214	253987.16	512	592	forward 2	TM
215	344553.1	3343	3420	forward 1	TM
216	410785.1	2055	2141	forward 3	TM
216	410785.1	4411	4494	forward 1	TM
216	410785.1	997	1080	forward 1	SP
216	410785.1	1383	1469	forward 3	TM
216	410785.1	4554	4637	forward 3	TM
217	237623.6	24	104	forward 3	SP
219	1099500.15	10	102	forward 1	TM
222	2278688CD1	1	39		SP
223	380283.1	6996	7079	forward 3	TM
223	380283.1	73	153	forward 1	SP
223	380283.1	3502	3591	forward 1	SP
223	380283.1	7939	8019	forward 1	TM
223	380283.1	6383	6460	forward 2	TM
223	380283.1	6479	6562	forward 2	TM
223	380283.1	6083	6175	forward 2	SP
228	3478236CD1	1	26		SP
228	3478236CD1	191	217		SP
229	147541.17	4089	4178	forward 3	SP
233	413268.6	4424	4513	forward 2	SP
233	413268.6	3689	3772	forward 2	SP
233	413268.6	893	979	forward 2	SP
238	420527.25	660	737	forward 3	TM
238	420527.25	662	742	forward 2	TM
240	474165.26	2961	3074	forward 3	SP
240	474165.26	3015	3098	forward 3	TM
243	346209.3	3564	3650	forward 3	SP
249	481231.17	1760	1846	forward 2	SP
250	1045853.2	1238	1324	forward 2	SP
253	085282.1	339	422	forward 3	TM
258	2636043CD1	117	143		TM
262	240518.34	1591	1701	forward 1	SP
266	253783.3	1181	1264	forward 2	SP
266	253783.3	1181	1264	forward 2	SP
268	902559.1	4378	4464	forward 1	SP
268	902559.1	512	607	forward 2	SP
276	474691.3	1030	1107	forward 1	SP
276	474691.3	3859	3945	forward 1	TM
276	474691.3	3957	4040	forward 3	TM
283	1040190.3	81	164	forward 3	SP
287	1095604.1	182	262	forward 2	SP
288	241291.28	10604	10684	forward 2	SP
288	241291.28	73	153	forward 1	SP
288	241291.28	4075	4176	forward 1	SP
288	241291.28	11296	11373	forward 1	TM
288	241291.28	10088	10168	forward 2	SP
288	241291.28	10841	10921	forward 2	TM
288	241291.28	3228	3311	forward 3	SP

288	241291.28	655	738	forward 1	SP
294	400253.5	1917	1994	forward 3	SP
294	400253.5	748	828	forward 1	SP
294	400253.5	1063	1152	forward 1	SP
294	400253.5	1963	2040	forward 1	SP
294	400253.5	213	293	forward 3	SP
305	1097910.1	204	284	forward 3	SP
305	1097910.1	582	662	forward 3	SP
306	246841.1	2036	2137	forward 2	SP
307	351241.1	139	219	forward 1	TM
311	2253717CD1	1	27		SP
315	232818.15	204	290	forward 3	SP
315	232818.15	782	862	forward 2	TM
322	478620.53	306	386	forward 3	SP
322	478620.53	227	313	forward 2	SP
322	478620.53	1135	1227	forward 1	SP
325	474588.21	1315	1392	forward 1	TM
328	347796.7	2467	2550	forward 1	TM
334	995575.17	1691	1771	forward 2	SP
334	995575.17	1641	1727	forward 3	TM
334	995575.17	3283	3363	forward 1	TM
337	413864.17	1178	1258	forward 2	TM
337	413864.17	1159	1239	forward 1	TM
350	235447.5	5478	5558	forward 3	TM
351	331104.2	2656	2754	forward 1	SP
356	480375.28	54	134	forward 3	TM
356	480375.28	50	130	forward 2	TM
356	480375.28	54	134	forward 3	TM
356	480375.28	50	130	forward 2	TM
357	364726.10	1380	1466	forward 3	SP
358	364726.12	4106	4183	forward 2	TM
361	903508.12	2552	2632	forward 2	TM
363	346716.21c	529	609	forward 1	SP
367	1719478CD1	1734	1760		TM
367	1719478CD1	1631	1656		TM
367	1719478CD1	380	407		TM
367	1719478CD1	1627	1653		SP
367	1719478CD1	939	967		SP
371	980446.1	353	427	forward 2	TM
373	1102297.22	173	256	forward 2	SP
373	1102297.22	1838	1924	forward 2	SP
374	215112.1	383	466	forward 2	TM
375	171495.1	1008	1097	forward 3	TM
378	5834958CD1	408	435		TM
378	5834958CD1	488	518		SP
378	5834958CD1	373	402		SP
380	333840.1	1873	1950	forward 1	TM
380	333840.1	2180	2269	forward 2	SP
380	333840.1	1818	1901	forward 3	SP
386	246727.17	2262	2348	forward 3	SP
388	1102322.18	155	247	forward 2	SP
397	372647.1	215	295	forward 2	TM
399	209279.1	661	741	forward 1	SP

TABLE 6

SEQ ID N	O: TEMPLATE	I CLONE ID	START	STOP
1	220060.4	26474	<u>,</u> 1	274
2	016238.1	60123	1	218
3	1266683.1	63038	1	212
4	129384.1c	72713	225	440
5	3201389CB1	85606	1	2537
7	086390CB1	86390	23	647
9	1102322.16	118501	280	852
10	1545176CB1	118501	36	2295
12	978222.4	121785	764	1167
13	978222.5	121785	92	636
14	1720920CB1	136073	71	7699
16	1857017CB1	160822	334	4843
16	1857017CB1	3493710	334	4843
18	2114865CB1	167081	369	1949
20	2700132CB1	172023	70	10502
20	2700132CB1	2470485	70 70	10502
22	238349.2	211389	70 4294	4448
23	238349.4c	211389	1	
24	402917.3c	237027	428	110 858
25	406330.1	259054	482	
26	2516070CB1	271299	757	1179 1693
26	2516070CB1	2517386	757 757	
28	167507CB1	279249	1	1693
30	3860413CB1	279249	1	1656
30	3860413CB1	3121871		617
32	3393861CB1	280932	1 28	617
34	2517374CB1	293477	28 16	1656
36	030850.7	311346	10	868 483
37	237416.12c	318486	1	463 567
38	237416.126	318486	93	616
39	1269631CB1	341884	118	6985
41	961189CB1	348143	25	2192
43	246946.1	388964	0	394
44	017958.1	389362	1	259
45	985556.1	407032	906	1234
46	476301CB1	408886	1	2523
48	996427.2	419492	801	2458
49	2989375CB1	437481	1	902
51	236359.2	442723	112	618
52	011112.1c	443991	12	342
53	198268.1	450856	297	854
54	978740.3	452321	2764	3535
55	400197.1	454839	1	1025
56	235687.5c	459372	-27	410
57	2797839CB1	460779	1	2650
59	978690.6	462069	164	864
60	348072.5	480791	1960	2765
61	085596CB1	481402	119	2070
63	103917CB1	510056	39	1674
		-	- -	~ ~ / .

65	3603037CB1	511448	1	2979
67	088564CB1	560115	.1	823
69	040429.1	604019	736	1087
70	407096.2	630625	2268	3868
71	209265.54	669498	2155	2752
72	701484CB1	701484	-188	2308
74	251859.2	758192	654	3262
75	3766715CB1	773154	1666	5251
77	2049950CB1	818192	347	3779
79	231588.6c	818192	1	557
80	152298.2	872017	84	834
81	199507.1	891322	1	342
82	1434821CB1	963536	-298	620
84	289671.27	970905	2307	2723
85	1282225CB1	990375	130	657
87	263336.57	1213932	4	324
88	464689.40	1259841	1	897
89	155943.1	1272483	339	840
90	243794.19c	1306814	834	1050
91	243794.23	1306814	284	522
92	159309CB1	1308112	21	3061
94	1273641CB1	1315663	127	1425
96	403717.1	1316801	1	773
97	047593.1	1326255	1	794
98	347055.4	1368834	3159	3550
99	898899.11	1379063	1046	1377
100	898899.32	1379063	2052	2524
101	2047630CB1	1381654	180	2123
103	1039889.8	1395143	609	994
104	1272969CB1	1435374	2984	4434
106	282397.85c	1441245	2665	6228
107	282397.94	1441245	1	622
108	1448817CB1	1448718	15	1535
110	1100769.2	1454436	35	697
111	332521.1	1457424	871	1424
112	225080.16	1457718	4047	4330
113	334851.5	1464613	757	1127
114	995529.7	1468660	445	843
115	995529.8	1468660	938	1169
116	201851.1	1482116	3045	3958
117	059509CB1	1495382	16	1623
119	481231.14	1500245	1	406
120	280276CB1	1511658	112	2332
122	4675668CB1	1519431	17	1723
124	153825.1	1519683	560	1056
125	403484.2c	1522880	1695	2180
126	1459432CB1	1522880	1	2144
128	1096583.1	1530595	233	424
129	516300CB1	1559665	1	763
131	627856CB1	1559756	550	1997

133	1823159CB1	1560906	1	3471
135	232567.4	1577614	513	1142
136	218419.1	1616783	i	184
137	1630551CB1	1619292	2	1229
139	360961.19	1619980	1208	1470
140	809809CB1	1623214	1	2116
142	2558815CB1	1630990	-4	2431
144	242010.16	1696224	1767	2352
145	1678695CB1	1696224	-761	1690
147	988653.1	1705208	1702	2382
148	1250434CB1	1711151	46	3277
150	236196.3	1732221	1	524
151	442308.1	1756875	1	375
152	060957.1	1786554	1	597
153	014284CB1	1822716	2	1900
155	1095192.1	1833362	247	684
156	233003.20	1834236	1	552
157	1911808CB1	1834236	88	3722
159	978276.8	1838114	3037	3497
160	405844.21	1845046	341	938
161	405844.22	1845046	925	1484
162	2705515CB1	1846209	1	2256
164	2023119CB1	1846463	34	3324
166	1000084.27	1861456	1583	1991
166	1000084.27	3679667	1646	2138
167	220134.1	1867614	477	2949
168	216331.1	1869130	1226	1976
169	206044.1	1871340	347	580
170	382906.16	1874037	54	505
171	331306.1	1874307	1576	2007
172	1094829.20	1890576	1268	1652
173	1094829.38	1890576	566	1023
174	1135580.4	1890791	3964	5687
175	196623.3	1920215	1299	1746
176	048488.32	1922468	2741	3572
177	2767012CB1	1926883	17	1485
179	1651724CB1	1930235	41	2059
181	206397.1	1956982	1	237
182	461707.40	1958226	353	701
183	2706645CB1	1963081	13	975
185	474372.7	1966517	2037	2539
186	3592543CB1	1969563	1	2198
188	048612.12c	1975268	872	1420
189	048612.13	1975268	2418	2666
190	245259.16	1998269	1787	2319
191	522433CB1	2042056	15	1251
193	1040667.43	2046717	1	372
194	2048551CB1	2048551	1	558
196	1969731CB1	2055569	3	3038
198	1326983.14	2055867	4029	4749
			. 323	., .,

199	2120743CB1	2120743	1	3934
201	3551330CB1	2121863	334	770
203	1440032CB1	2123516	622	2962
205	1000133.1	2132285	137	609
206	4020439CB1	2132774	260	700
208	2507087CB1	2160794	1	4241
210	239996.1	2195427	127	589
211	1097380.1	2201708	43	967
212	021524.2c	2208780	3082	3404
213	021524.9	2208780	1272	1527
214	253987.16	2232658	1	360
215	344553.1	2234853	2584	3171
216	410785.1	2241825	4508	4883
217	237623.6	2242817	1	451
218	076047.1	2252107	1	392
219	1099500.15	2273944	1107	
220	1099500.18	2273944	2360	1756
221	2278688CB1	2278688	1233	2777
223	380283.1	2293496	7546	5389
224	1720847CB1	2311213	855	7928
226	333776.1c	2311213		1844
227	3478236CB1	2352645	126	201
229	147541.17	2352645	1	1278
230	331120.16c		1850	3484
231	575983CB1	2365335 2382192	4150	4601
233	413268.6		1	798
234	1989186CB1	2382195 2383269	2182	4148
236	337448.1c	2394990	904 1	3033
237	228304.19	2394990	636	308
238	420527.25	2446289	248	1144
239	998034.3	2448149	377	2143
240	474165.26	2453558		3629
241	697785CB1	2495131	105	560
243	346209.3	2511277	233 3331	770
244	167772CB1	2513883	505	3758 974
246	2514988CB1	2514988		
248	481231.16	2514988	199 57	1492
249	481231.17	2516070	205	461 1661
249	481231.17	2516104	819	
249	481231.17	2516164	197	1661
249	481231.17	2516261		1659
250	1045853.2	2517254	1395	1698
250	1045853.2	5398014	1874	3884
251	336615.1	2520894	1874	3898
252	1328423.2	2527879	1088	1325
253	085282.1	2545486	423 83	938
254	1081605.3	2545486 2550767	83 3196	487
255	1053517.1	2579218		3739
256	480169.76	2607921	1 716	233
257	2636043CB1	2636043	98	2565
201	2030043CD1	2030043	76	1101

259	2993696CB1	2641522	-8	2532
261	240518.21	2660756	1	333
262	240518.34	2660756	534	1026
263	001322.4c	2663164	1069	3206
264	350502.3	2675232	39	440
265	350502.4c	2675232	547	1016
266	253783.3	2695371	993	1843
267	085119.1	2708055	577	869
268	902559.1	2740665	5148	5635
269	4113161CB1	2756333	108	2295
271	2757583CB1	2757583	268	709
273	198317.1	2765271	29	881
274	1508254CB1	2769888	1363	4652
276	474691.3	2813255	820	1466
277	2457215CB1	2820337	1	3437
279	201395.4c	2822027	4780	5689
280	233189.21	2825358	85	565
281	196606.6c	2830828	1	566
282	196606.8c	2830828	113	696
283	1040190.3	2831490	38	1110
284	1427459CB1	2860918	-28	1364
286	480453.16c	2879068	2710	3067
287	1095604.1	2884613	3	282
288	241291.28	2890336	2125	2463
289	230611.1	2891601	1	64
290	3993708CB1	2899419	59	633
292	1000133.12	2899419	13	307
293	400253.17c	2912637	4051	4601
294	400253.5	2912637	238	742
295	030882CB1	2912830	67	443
297	898779CB1	2921194	294	1408
299	3727408CB1	2921991	4	532
301	984236.1c	2925373	47	494
302	984236.2c	2925373	223	494
303	348082.5	2929484	193	582
304	348082.7	2929484	516	980
305	1097910.1	2933775	389	886
306	246841.1	2953987	2907	3189
307	351241.1	2955163	312	757
308	2790762CB1	2956444	158	1221
310	2253717CB1	2957205	103	815
312	2655184CB1	2991027	401	1496
314	363000.9c	2991027	1014	1447
315	232818.15	2992044	1069	1721
316	347781.10	2999855	576	937
317	2477616CB1	2999855	1	2835
319	360532.1	3026540	210	800
320	360532.9	3026540	79	1158
321	110245.1	3028719	1	396
322	478620.53	3038508	1447	1779

323	1813444CB1	3038508	7	1694
325	474588.21	3070625	1761	2181
326	407838.1	3074113	234	997
327	994387.19	3084204	1	509
328	347796.7	3108506	395	687
329	406498.4c	3109384	112	525
330	3346307CB1	3120209	2	1747
332	4005778CB1	3121380	208	1220
334	995575.17	3123731	2033	2944
335	863406CB1	3128810	62	4366
337	413864.17	3129338	1	1603
338	350106.16	3136857	1045	1577
339	399785.1	3158828	199	627
340	010498.19	3170010	3434	4175
341	255824.39	3208425	258	755
342	2706606CB1	3208425	347	1869
344	118006.1	3222802	1	162
345	1039889.26	3225977	64	1971
346	481480.7	3240708	1	392
347	662575CB1	3272165	17	1864
349	027619.3	3284411	5	813
350	235447.5	3345528	8274	8706
351	331104.2	3380034	2256	3067
352	348390.2	3381870	50	205
353	127004.1	3407653	1	640
354	026190.1	3427373	970	1345
355	250330.1	3472927	1	554
356	480375.28	3493381	100	548
357	364726.10	3494714	1	498
358	364726.12	3494714	3939	4473
359	1505038CB1	3606046	7	3701
361	903508.12	3715059	1589	2966
362	346716.17c	3792988	6200	6704
363	346716.21c	3792988	55	705
364	330776.1	3815422	2049	2357
365	407999.1c	4019706	1	368
366	1719478CB1	4066764	1	6348
368	351157.2	4070979	59	653
369	088957CB1	4087621	1888	4200
369	088957CB1	5398701	1888	4200
371	980446.1	4091186	1	801
372	198827.1	4092112	90	1147
373	1102297.22	4107126	1584	1682
374	215112.1	4110976	1	522
375	171495.1	4203937	51	1219
376	242010.43	4246966	150	335
377	5834958CB1	4254855	1	2919
379	335648.1c	4284384	33	430
380	333840.1	4287327	1166	1659
381	480885.2	4403805	190	2066

382	998106.8c	4508879	15	869
383	400701.4	4549259	.1	449
384	1100320.4	4556538	14	796
385	246727.11	4715924	272	642
386	246727.17	4715924	1249	1618
387	1102322.12c	4721130	207	672
388	1102322.18	4721130	844	1068
389	2070610CB1	4795635	249	1680
391	336733.3	5047895	1	420
392	1326902.13	5077219	105	580
393	1326902.6	5077219	983	1443
394	013521.16	5093071	312	767
395	985369.1	5102731	337	1131
396	002455.1	5266015	670	1134
397	372647.1	5266376	81	792
398	208075.1	5293028	417	737
399	209279.1	5399371	2090	2521
400	381058.1	5512044	1	517
401	046977.1	5541949	1	308

1 220060 4 3 1266683.1 4 129384 1c 9 110232.16 12 97822.2 4 13 97822.2 5 23 238349.4c 24 402917.3c 25 406330.1 37 237416.12c 38 237416.12c 39 237416.12c 39 237416.12c 39 237416.12c 30 37416.12c 30 37416.12c 30 37416.12c 31 23638.2 32 235687.5c 32 235687.5c 32 335687.5c 34 607096 2 37 209265.54 37 209265.54 38 199507.1 38 289671.27 38 464689.40	Liver - 35%, Sense Organs - 28%, Nervous System - 14% Embryonic Structures - 100% Skin - 64%, Respiratory System - 14%, Henie and Immune System - 14% Skin - 12%, Sense Organs - 11% Germ Cells - 42%, Unclassified/Mixed - 15%, Musculoskeletal System - 10%, Female Genitalia - 10% Connective Tissue - 18%, Male Genitalia - 18%, Musculoskeletal System - 10%, Female Genitalia - 18%, Musculoskeletal System - 15% Hemic and Immune System - 10% Digestive System - 42%, Uninary Tract - 40% Germ Cells - 64%, Nervous System - 36% Unclassified/Mixed - 93% Exocrine Glands - 17%, Liver - 16%, Female Genitalia - 14% Female Genitalia - 86%, Hemic and Immune System - 10% Hemic and Immune System - 29%, Respiratory System - 13% Hemic and Immune System - 82%, Male Genitalia - 18% Sense Organs - 14%, Germ Cells - 11% Sense Organs - 14%, Germ Cells - 11% Sense Organs - 14%, Germ Cells - 11% Sense Organs - 13%, Embryonic Structures - 12%
	Germ Cells - 42%, Unclassified/Mixed - 15%, Musculoskeletal System - 10%, Female Genitalia - 10% Connective Tissue - 18%, Male Genitalia - 18%, Musculoskeletal System - 15% Embryonic Structures - 17% Hemic and Immune System - 100% Digestive System - 42%, Urinary Tract - 40% Germ Cells - 64%, Nervous System - 36% Unclassified/Mixed - 93% Exocrine Glands - 17%, Liver - 16%, Female Genitalia - 14% Female Genitalia - 86%, Hemic and Immune System - 10% Hemic and Immune System - 29%, Respiratory System - 13% Hemic and Immune System - 19%, Exocrine Glands - 13%, Respiratory System - 46% Hemic and Immune System - 82%, Male Genitalia - 18% Sense Organs - 14%, Germ Cells - 11% Skin - 37%, Panercas - 13%, Embryonic Structures - 12% Skin - 37%, Panercas - 13%, Embryonic Structures - 12%
	Connective Tissue - 18%, Mate Genitalia - 18%, Musculoskeletal System - 15% Embryonic Structures - 17% Hemic and Immune System - 100% Digestive System - 42%, Urinary Tract - 40% Germ Cells - 64%, Nervous System - 36% Unclassified/Mixed - 93% Exocrine Glands - 17%, Liver - 16%, Female Genitalia - 14% Female Genitalia - 86%, Hemic and Immune System - 10% Hemic and Immune System - 29%, Respiratory System - 13% Hemic and Immune System - 19%, Exocrine Glands - 13%, Respiratory System - 46% Hemic and Immune System - 82%, Male Genitalia - 18% Sense Organs - 14%, Germ Cells - 11% Skin - 37%, Pancreas - 13%, Embryonic Structures - 12%
	Embryonic Structures - 17% Hemic and Imnune System - 100% Digestive System - 42%, Urinary Tract - 40% Genn Cells - 64%, Nervous System - 36% Unclassified/Mixed - 93% Exocrine Glands - 17%, Liver - 16%, Fenale Genitalia - 14% Female Genitalia - 86%, Hemic and Immune System - 10% Hemic and Immune System - 29%, Respiratory System - 13% Hemic and Immune System - 19%, Exocrine Glands - 13%, Respiratory System - 12% Connective Tissue - 54%, Hemic and Immune System - 46% Hemic and Immune System - 82%, Male Genitalia - 18% Sense Organs - 14%, Germ Cells - 11% Skin - 37%, Pancreas - 13%, Embryonic Structures - 12%
	Hemic and Innuune System - 100% Digestive System - 42%, Urinary Tract - 40% Germ Cells - 64%, Nervous System - 36% Unclassified/Mixed - 93% Exocrine Glands - 17%, Liver - 16%, Female Genitalia - 14% Female Genitalia - 86%, Hemic and Immune System - 10% Hemic and Immune System - 29%, Respiratory System - 13% Hemic and Immune System - 19%, Exocrine Glands - 13%, Respiratory System - 12% Connective Tissue - 54%, Hemic and Immune System - 46% Hemic and Immune System - 82%, Male Genitalia - 18% Sense Organs - 14%, Germ Cells - 11% Skin - 37%, Pancreas - 13%, Embryonic Structures - 12%
	Digestive System - 42%, Urinary Tract - 40% Germ Cells - 64%, Nervous System - 36% Unclassified/Mixed - 93% Exocrine Glands - 17%, Liver - 16%, Female Genitalia - 14% Female Genitalia - 86%, Hemic and Immune System - 10% Hemic and Immune System - 29%, Respiratory System - 13% Hemic and Immune System - 19%, Exocrine Glands - 13%, Respiratory System - 12% Connective Tissue - 54%, Hemic and Immune System - 46% Hemic and Immune System - 82%, Male Genitalia - 18% Sense Organs - 14%, Germ Cells - 11% Skin - 37%, Pancreas - 13%, Embryonic Structures - 12%
	Gernn Cells - 64%, Nervous System - 36% Unclassified/Mixed - 93% Exocrine Glands - 17%, Liver - 16%, Female Genitalia - 14% Female Genitalia - 86%, Hemic and Immune System - 10% Hemic and Immune System - 19%, Exocrine Glands - 13%, Respiratory System - 12% Connective Tissue - 54%, Hemic and Immune System - 46% Hemic and Immune System - 82%, Male Genitalia - 18% Sense Organs - 14%, Germ Cells - 11% Skin - 37%, Pancreas - 13%, Embryonic Structures - 12%
	Unclassified/Mixed - 93% Exocrine Glands - 17%, Liver - 16%, Female Genitalia - 14% Female Genitalia - 86%, Hemic and Immune System - 10% Hemic and Immune System - 29%, Respiratory System - 13% Hemic and Immune System - 19%, Exocrine Glands - 13%, Respiratory System - 12% Connective Tissue - 54%, Hemic and Immune System - 46% Hemic and Immune System - 82%, Male Genitalia - 18% Sense Organs - 14%, Germ Cells - 11% Skin - 37%, Pancreas - 13%, Embryonic Structures - 12%
	Exocrine Glands - 17%, Liver - 16%, Female Genitalia - 14% Female Genitalia - 86%, Hemic and Immune System - 10% Hemic and Immune System - 29%, Respiratory System - 13% Hemic and Immune System - 19%, Exocrine Glands - 13%, Respiratory System - 12% Connective Tissue - 54%, Hemic and Immune System - 46% Hemic and Immune System - 82%, Male Genitalia - 18% Sense Organs - 14%, Germ Cells - 11% Skin - 37%, Pancreas - 13%, Embryonic Structures - 12%
	Female Genitalia - 86%, Henric and Immune System - 10% Hemic and Immune System - 29%, Respiratory System - 13% Hemic and Immune System - 19%, Exocrine Glands - 13%, Respiratory System - 12% Connective Tissue - 54%, Henric and Immune System - 46% Hemic and Immune System - 82%, Male Genitalia - 18% Sense Organs - 14%, Germ Cells - 11% Skin - 37%, Pancreas - 13%, Embryonic Structures - 12%
	Hemic and Immune System - 29%, Respiratory System - 13% Hemic and Immune System - 19%, Exocrine Glands - 13%, Respiratory System - 12% Connective Tissue - 54%, Hemic and Immune System - 46% Hemic and Immune System - 82%, Male Genitalia - 18% Sense Organs - 14%, Germ Cells - 11% Skin - 37%, Pancreas - 13%, Embryonic Structures - 12%
	Hemic and Immune System - 19%, Exocrine Glands - 13%, Respiratory System - 12% Connective Tissue - 54%, Hemic and Immune System - 46% Hemic and Immune System - 82%, Male Genitalia - 18% Sense Organs - 14%, Germ Cells - 11% Skin - 37%, Pancreas - 13%, Embryonic Structures - 12%
	Connective Tissue - 54%, Henric and Immune System - 46% Henric and Immune System - 82%, Male Genitalia - 18% Sense Organs - 14%, Germ Cells - 11% Skin - 37%, Pancreas - 13%, Embryonic Structures - 12%
	Hemic and Immune System - 82%, Male Genitalia - 18% Sense Organs - 14%, Germ Cells - 11% Skin - 37%, Pancreas - 13%, Embryonic Structures - 12%
	Sense Organs - 14%, Germ Cells - 11% Skin - 37%, Pancreas - 13%, Embryonic Structures - 12%
	Skin - 37%, Pancreas - 13%, Embryonic Structures - 12%
	Germ Cells - 44%, Skin - 23%, Unclassified/Mixed - 16%
	Unclassified/Mixed - 33%, Nervous System - 21%, Respiratory System - 19%
-	Liver - 90%
	Connective Tissue - 15%
	Germ Cells - 27%, Musculoskeletal System - 11%
	Respiratory System - 25%, Female Genitalia - 25%, Nervous System - 17%, Digestive System - 17%, Hemic and Immune System - 17%
	Respiratory System - 60%, Digestive System - 40%
	Nervous System - 50%, Digestive System - 50%
	Sense Organs - 26%, Urinary Tract - 19%
	Liver - 23%, Urinary Tract - 17%, Hemic and Immune System - 17%
	Female Genitalia - 13%, Liver - 11%
	Unclassified/Mixed - 33%, Germ Cells - 30%
90 243794.19c	Stornatognathic System - 14%
96 403717.1	Unclassified/Mixed - 44%, Embryonic Structures - 21%, Urmary Tract - 19%
98 347055.4	Skin - 15%, Liver - 12%
11.668868 66	Liver - 41%, Respiratory System - 14%, Pancreas - 12%
100 898899.32	Liver - 62%, Urinary Tract - 12%
106 282397.85c	Embryonic Structures - 11%

FUUEZON CENETED TABLE 7

TABLE 7

Skin - 45%, Connective Tissue - 23%, Hemic and Immune System - 19% Sense Organs - 14%, Embryonic Structures - 11%	Urinary Tract - 27%, Cardiovascular System - 18%, Musculoskeletal System - 14%	Digestive System - 38%, Liver - 19%, Pancreas - 18%	Liver - 53%, Heinic and Immune System - 14%, Urinary Tract - 12% Dioestive System - 38% Pancraas - 10% Resentations System - 11%	Stomatognathic System - 11%	Nervous System - 11%	Embryonic Structures - 31%, Endocrine System - 13%	Hemic and Immune System - 71%, Male Genitalia - 29%	Sense Organs - 12%	Liver - 13%, Germ Cells - 12%, Unclassified/Mixed - 11%	Stomatognathic System - 11%	Unclassi fied/Mixed - 49%, Germ Cells - 23%, Male Genitalia - 14%	Liver - 42%, Unclassified/Mixed - 10%	Sense Organs - 12%	Germ Cells - 23%	Digestive System - 24%, Pancreas - 12%	Liver - 83%, Digestive System - 12%	Liver - 70%, Digestive System - 14%	Liver - 93%	Sense Organs - 57%, Endocrine System - 15%, Unclassified/Mixed - 11%	Endocrine System - 17%, Embryonic Structures - 11%	Unclassified/Mixed - 26%, Endocrine System - 16%, Male Genitalia - 13%	Urinary Tract - 100%	Liver - 26%, Respiratory System - 19%, Connective Tissue - 17%	Pancreas - 10%	Connective Tissue - 44%, Cardiovascular System - 25%, Urinary Tract - 25%	Exocrine Glands - 28%, Urinary Tract - 28%, Cardiovascular System - 14%	Male Genitalia - 30%, Urinary Tract - 27%, Nervous System - 24%	Digestive System - 12%, Exocrine Glands - 11%, Urinary Tract - 10%	Musculoskeletal System · 16%, Exocrine Glands - 15%, Embryonic Structures - 12%, Unclassified/Mixed - 12%	Germ Cells - 14%	Nervous System - 38%, Endocrine System - 14%	Liver - 30%	Hemic and Immune System - 100%	Sense Organs - 11%, Connective Tissue - 11%	Hemic and Immune System - 37%, Germ Cells - 13%
239996.1 1097380.1	253987.16	344553.1	237623.6	1099500.15	1099500.18	380283.1	333776.1c	147541.17	331120 16c	413268.6	337448.1c	228304.19	420527 25	998034.3	346209.3	481231.16	481231.17	1045853.2	336615.1	1328423.2	1081605.3	1053517.1	240518.21	240518 34	350502.3	350502.4c	253783 3	902559.1	198317.1	474691.3	201395.4c	233189.21	196606.6c	196606.8c	1040190.3
210	214	215	217	219	220	223	226	229	230	233	236	237	238	239	243	248	249	250	251	252	254	255	261	262	264	265	566	268	273	276	279	280	281	282	283

TABLE 7

Urinary Tract - 10%

480453.16c 1095604.1

007	4004.33.100	Olinaly Hact - 10%
287	1095604 1	Skin - 28%, Embryonıc Structures - 19%, Endocrine System - 14%
289	230611.1	Respiratory System - 60%, Hemic and Immune System - 40%
292	1000133.12	Cardiovascular System - 15%
293	400253 17c	Germ Cells - 31%
294	400253.5	Liver - 41%, Urinary Tract - 19%, Exocrine Glands - 19%
301	984236 lc	Digestive System - 35%, Liver - 30%, Female Genitalia - 14%
302	984236 2c	Digestive System - 72%, Exocrine Glands - 22%
303	348082 5	Connective Tissue - 36%, Germ Cells - 19%
304	348082 7	Embryonic Structures - 38%, Skin - 23%, Digestive System - 10%
305	1097910.1	Liver - 48%, Male Genitalia - 20%, Endocrine System - 11%
306	246841.1	Sense Organs - 30%
307	3512411	Urinary Tract - 36%, Hemic and Immune System - 36%, Musculoskeletal System - 27%
315	232818 15	Skin - 12%
316	347781.10	Skin - 20%
319	360532.1	Stomatognathic System - 67%, Musculoskeletal System - 16%, Cardiovascular System - 12%
320	3605329	Musculoskeletal System - 49%, Cardiovascular System - 22%, Sense Organs - 11%
321	110245 1	Cardiovascular System - 67%, Hemic and Immune System - 33%
325	474588 21	Female Genitalia - 17%, Respiratory System - 15%, Embryonic Structures - 13%
326	407838.1	Musculoskeletal System - 60%, Respiratory System - 30%, Nervous System - 10%
327	994387.19	Female Genitalia - 75%, Nervous System - 25%
328	347796 7	Stomatognathic System - 13%
329	406498.4c	Sense Organs - 75%, Unclassified/Mixed - 14%
334	995575 17	Scnse Organs - 14%
337	413864 17	Liver - 18%, Respiratory System - 12%, Exocrine Glands - 11%
339	399785 1	Pancreas - 31%, Unclassified/Mixed - 31%, Male Genitalia - 16%
341	255824.39	Stomatognathic System - 15%, Musculoskeletal System - 13%
344	118006.1	Digestive System - 100%
346	481480 7	Digestive System - 100%
350	235447 5	Embryonic Structures - 11%, Liver - 11%
351	3311042	Liver - 64%, Hemic and Immune System - 10%
352	348390 2	Digestive System - 46%, Female Genitalia - 21%, Male Genitalia - 20%
353	127004 1	Germ Cells - 84%
355	250330 1	Hemic and Immune System - 63%, Respiratory System - 38%
356	480375 28	Musculoskeletal System - 46%, Endocrine System - 38%, Male Genitalia - 15%
357	364726.10	Sense Organs - 39%
358	364726.12	Sense Organs - 15%, Unclassified/Mixed - 14%
361	903508.12	Embryonic Structures - 35%, Germ Cells - 15%, Liver - 14%

ngalanza ny zant

TABLE 7

Unclassified/Mixed - 23%, Germ Cells - 11%, Hemic and Immune System - 10%	Cardiovascular System - 18%, Nervous System - 18%, Endocrine System - 13%, Male Genitalia - 13%	Sense Organs - 17%, Connective Tissue - 15%	Nervous System - 100%	Urinary Tract - 80%, Hemic and Immune System - 20%	Embryonic Structures - 31%, Nervous System - 16%, Connective Tissue - 11%, Male Genitalia - 11%	Connective Tissue - 25%, Nervous System - 17%, Exocrine Glands - 11%	Male Genitalia - 83%, Nervous System - 17%	Unclassified/Mixed - 43%, Cardiovascular System - 18%, Respiratory System - 14%	Musculoskeletal System - 21%, Nervous System - 20%	Liver - 72%, Exocrine Glands - 18%	Liver - 71%, Urinary Tract - 20%	Connective Tissue - 14%, Male Genitalia - 14%	Unclassified/Mixed - 36%, Respiratory System - 26%	Nervous System - 43%, Endocrine System - 36%, Female Genitalia - 21%	Nervous System - 10%, Skin - 10%, Respiratory System - 10%, Endocrine System - 10%	Embryonic Structures - 26%, Connective Tissue - 21%, Male Genitalia - 15%	Sense Organs - 13%	Musculoskeletal System - 41%, Hemic and Immune System - 34%	Sense Organs - 25%, Connective Tissue - 10%	Cardiovascular System - 25%, Embryonic Structures - 25%, Skin - 13%	Musculoskeletal System - 25%, Pancreas - 19%, Digestive System - 13%	Connective Tissue - 12%	Germ Cells - 16%, Male Genitalia - 12%	Nervous System - 100%	Hemic and Immune System - 28%, Unclassified/Mixed - 20%, Exocrine Glands - 13%	Liver - 76%	Male Genitalia - 67%, Nervous System - 33%
346716.17c	346716.21c	330776.1	407999.1c	351157.2	980446.1	198827.1	215112.1	171495.1	242010.43	335648.1c	333840.1	480885.2	998106.8c	400701.4	1100320.4	246727.11	246727.17	1102322.12c	1102322.18	336733.3	1326902.13	13269026	1 698586	372647 1	208075.1	209279 1	381058.1
362	363	364	365	368	371	372	374	375	376	379	380	381	382	383	384	385	386	387	388	391	392	393	395	397	398	399	400